



Docket No.

PATENT

154-01924

AUG 27 2002

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TECH CENTER 160012900

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANTS: Akio MATSUDA et al. CONF.: 6200
APPLN. NO.: 10/042,211 GROUP: 1646
FILED: January 11, 2002 EXAMINER: Unknown
FOR: NF- κ B ACTIVATING GENE

**LETTER SUBMITTING CERTIFIED COPY
OF PCT APPLICATION**

Assistant Commissioner of Patents
Washington, DC 20231

August 26, 2002

Sir:

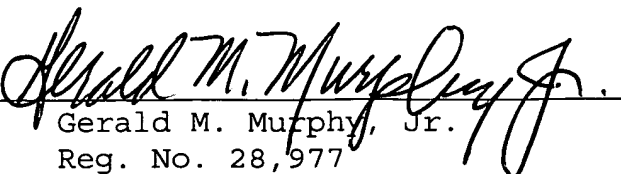
Attached hereto is a certified copy of PCT/JP01/11389, which was filed on December 25, 2001. The present application is a continuation of this PCT application, and priority is claimed on this PCT application under 35 USC 120. The present application (10/042,211) is identical to this PCT application, and the English translation of application 10/042,211, which was filed on May 20, 2002, is an English translation of PCT/JP01/11389.

The PTO is requested to place this certified copy of PCT/JP01/11389 in the file.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. §§1.16 or 1.17; particularly, extension of time fees.

Respectfully submitted,

BIRCH, STEWART, KOLASCH & BIRCH, LLP

By 
Gerald M. Murphy, Jr.
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Enclosure: Certified Copy of PCT/JP01/11389



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(Translation)

PATENT OFFICE
JAPANESE GOVERNMENT

This is to certify that the annexed is a true copy of
the following application as filed with this Office.

Date of Application: December 25, 2001

Application Number: PCT/JP01/11389

Applicant(s): Akio MATSUDA
Goichi HONDA
Shuji MURAMATSU
Yukiko NAGANO

February 22, 2002

Commissioner,
Patent Office

Kozo Oikawa (seal)

Certificate No. 14-500046



日 本 国 特 許
JAPAN PATENT OFFICE

TECH CENTER 1600/2900
AUG 27 2002

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Matsuda et al
18/042,211
filed 01-11-02
BSK, LLP
(703) 205-8000
1051

別紙添付の書類は下記の出願書類の謄本に相違ないことを証明する。
This is to certify that the annexed is a true copy of the following application as filed with this Office.

出 願 年 月 日
Date of Application: 2001年12月25日

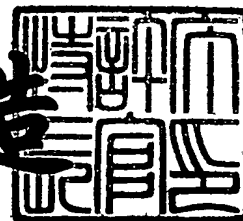
出 願 番 号
Application Number: PCT/JPO1/11389

出 願 人
Applicant (s): 松田 昭生
本田 剛一
村松 周治
長野 由希子

2002 年 2 月 22 日

特許庁長官
Commissioner,
Japan Patent Office

及川耕造



出証平 14-500046

受理官庁用写し

1/5

特許協力条約に基づく国際出願願書

PH-1456-PCT

原本（出願用） - 印刷日時 2001年12月25日（25. 12. 2001）火曜日 14時36分25秒

0	受理官庁記入欄	PCT/JP 01/11389
0-1	国際出願番号.	
0-2	国際出願日	25.12.01
0-3	(受付印)	PCT International Application 日本国特許庁
0-4	様式-PCT/RO/101 この特許協力条約に基づく国際出願願書は、	
0-4-1	右記によって作成された。	PCT-EASY Version 2.92 (updated 01.03.2001)
0-5	申立て 出願人は、この国際出願が特許協力条約に従って処理されることを請求する。	
0-6	出願人によって指定された受理官庁	日本国特許庁 (RO/JP)
0-7	出願人又は代理人の書類記号	PH-1456-PCT
I	発明の名称	N F - K B 活性化遺伝子
II	出願人	
II-1	この欄に記載した者は	出願人である (applicant only)
II-2	右の指定国についての出願人である。	米国を除くすべての指定国 (all designated States except US)
II-4ja	名称	旭化成株式会社
II-4en	Name	ASAHI KASEI KABUSHIKI KAISHA
II-5ja	あて名:	530-8205 日本国 大阪府 大阪市北区 堂島浜一丁目2番6号
II-5en	Address:	2-6, Dojimahama 1-chome, Kita-ku Osaka-shi, Osaka 530-8205 Japan
II-6	国籍 (国名)	日本国 JP
II-7	住所 (国名)	日本国 JP
II-8	電話番号	06-6347-3111
III-1	その他の出願人又は発明者	
III-1-1	この欄に記載した者は	出願人及び発明者である (applicant and inventor)
III-1-2	右の指定国についての出願人である。	米国のみ (US only)
III-1-4ja	氏名(姓名)	松田 昭生
III-1-4en	Name (LAST, First)	MATSUDA, Akio
III-1-5ja	あて名:	417-0061 日本国 静岡県 富士市 伝法3629-1-404
III-1-5en	Address:	3629-1-404, Denpo, Fuji-shi, Shizuoka 417-0061 Japan
III-1-6	国籍 (国名)	日本国 JP
III-1-7	住所 (国名)	日本国 JP

III-2 III-2-1	その他の出願人又は発明者 この欄に記載した者は	出願人及び発明者である (applicant and inventor) 米国のみ (US only)
III-2-2	右の指定国についての出願人である。	
III-2-4j a	氏名(姓名)	本田 剛一
III-2-4e n	Name (LAST, First)	HONDA, Goichi
III-2-5j a	あて名:	416-0945 日本国 静岡県 富士市 宮島655-9
III-2-5e n	Address:	655-9, Miyajima, Fuji-shi, Shizuoka 416-0945 Japan
III-2-6	国籍 (国名)	日本国 JP
III-2-7	住所 (国名)	日本国 JP
III-3 III-3-1	その他の出願人又は発明者 この欄に記載した者は	出願人及び発明者である (applicant and inventor) 米国のみ (US only)
III-3-2	右の指定国についての出願人である。	
III-3-4j a	氏名(姓名)	村松 周治
III-3-4e n	Name (LAST, First)	MURAMATSU, Shuji
III-3-5j a	あて名:	416-0931 日本国 静岡県 富士市 蓼原17-13
III-3-5e n	Address:	17-13, Tadewara, Fuji-shi, Shizuoka 416-0931 Japan
III-3-6	国籍 (国名)	日本国 JP
III-3-7	住所 (国名)	日本国 JP
III-4 III-4-1	その他の出願人又は発明者 この欄に記載した者は	出願人及び発明者である (applicant and inventor) 米国のみ (US only)
III-4-2	右の指定国についての出願人である。	
III-4-4j a	氏名(姓名)	長野 由希子
III-4-4e n	Name (LAST, First)	NAGANO, Yukiko
III-4-5j a	あて名:	410-8501 日本国 静岡県 沼津市 下河原町29-5
III-4-5e n	Address:	29-5, Shimogawara-cho, Numazu-shi, Shizuoka 410-8501 Japan
III-4-6	国籍 (国名)	日本国 JP
III-4-7	住所 (国名)	日本国 JP

特許協力条約に基づく国際出願願書

PH-1456-PCT

原本(出願用) - 印刷日時 2001年12月25日 (25. 12. 2001) 火曜日 14時36分25秒

IV-1	代理人又は共通の代表者、通知のあて名 下記の者は国際機関において右記のごとく出願人のために行動する。	代理人 (agent)
IV-1-1ja	氏名(姓名)	平木 祐輔
IV-1-1en	Name (LAST, First)	HIRAKI, Yusuke
IV-1-2ja	あて名:	105-0001 日本国 東京都 港区 虎ノ門一丁目17番1号 虎ノ門5森ビル 3階
IV-1-2en	Address:	Toranomon No.5 Mori Building Third Floor, 17-1, Toranomon 1-chome Minato-ku, Tokyo 105-0001 Japan
IV-1-3	電話番号	03-3503-8637
IV-1-4	ファクシミリ番号	03-3503-0414
V	国の指定	
V-1	広域特許 (他の種類の保護又は取扱いを求める場合には括弧内に記載する。)	AP: GH GM KE LS MW MZ SD SL SZ TZ UG ZW 及びハラレプロトコルと特許協力条約の締約国である他の国 EA: AM AZ BY KG KZ MD RU TJ TM 及びユーラシア特許条約と特許協力条約の締約国である他の国 EP: AT BE CH&LI CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR 及びヨーロッパ特許条約と特許協力条約の締約国である他の国 OA: BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG 及びアフリカ知的所有権機構と特許協力条約の締約国である他の国
V-2	国内特許 (他の種類の保護又は取扱いを求める場合には括弧内に記載する。)	AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH&LI CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
V-5	指定の確認の宣言 出願人は、上記の指定に加えて、規則4.9(b)の規定に基づき、特許協力条約のもとで認められる他の全ての国の指定を行う。ただし、V-6欄に示した国の指定を除く。出願人は、これらの追加される指定が確認を条件としていること、並びに優先日から15月が経過する前にその確認がなされない指定は、この期間の経過時に、出願人によって取り下げられたものとみなされることを宣言する。	
V-6	指定の確認から除かれる国	なし (NONE)

特許協力条約に基づく国際出願願書

PH-1456-PCT

原本（出願用） - 印刷日時 2001年12月25日（25. 12. 2001）火曜日 14時36分25秒

VI-1	先の国内出願に基づく優先権主張	
VI-1-1	出願日	2000年12月28日（28. 12. 2000）
VI-1-2	出願番号	特願2000-402288
VI-1-3	国名	日本国 JP
VI-2	先の国内出願に基づく優先権主張	
VI-2-1	出願日	2001年03月26日（26. 03. 2001）
VI-2-2	出願番号	特願2001-088912
VI-2-3	国名	日本国 JP
VI-3	先の国内出願に基づく優先権主張	
VI-3-1	出願日	2001年08月24日（24. 08. 2001）
VI-3-2	出願番号	特願2001-254018
VI-3-3	国名	日本国 JP
VI-4	優先権証明書送付の請求 上記の先の出願のうち、右記の番号のものについては、出願書類の認証謄本を作成し国際事務局へ送付することを、受理官庁に対して請求している。	VI-1, VI-2, VI-3
VII-1	特定された国際調査機関(ISA)	日本国特許庁 (ISA/JP)
VIII	申立て	申立て数
VIII-1	発明者の特定に関する申立て	-
VIII-2	出願し及び特許を与えられる国際出願日における出願人の資格に関する申立て	-
VIII-3	先の出願の優先権を主張する国際出願日における出願人の資格に関する申立て	-
VIII-4	発明者である旨の申立て（米国を指定国とする場合）	-
VIII-5	不利にならない開示又は新規性喪失の例外に関する申立て	-
IX	照合欄	用紙の枚数
IX-1	願書（申立てを含む）	5
IX-2	明細書（配列表を除く）	58
IX-3	請求の範囲	9
IX-4	要約	1
IX-5	図面	29
IX-7a	国際出願に含まれる用紙の枚数（明細書の配列表を除く）	102
IX-6	紙形式に追加されたコンピュータ読み取り可能な形式による明細書の配列表部分（実施細則第801号(a)(ii)）	735
IX-7	合計	837

R0

R0

明細書の配列表

[2 フルテキスト] R0

特許協力条約に基づく国際出願願書

PH-1456-PCT

原本（出願用） - 印刷日時 2001年12月25日（25.12.2001）火曜日 14時36分25秒

	添付書類	添付	添付された電子データ
IX-8	手数料計算用紙	✓	-
IX-11	包括委任状の写し	✓	-
IX-16	コンピュータ読み取り可能なヌクレオチド又はアミノ酸配列表		
IX-16 - (i)	規則13の3に基づき提出する 国際調査のための写し（国際 出願の一部を構成しない）	-	2 フレキシブルディスク
IX-17	PCT-EASYディスク	-	フレキシブルディスク
IX-18	その他	納付する手数料に相当する 特許印紙を貼付した書 面	-
IX-18	その他	国際事務局の口座へ振込 を証明する書面	-
IX-19	要約書とともに提示する図の 番号		
IX-20	国際出願の使用言語名:	日本語	
X-1	提出者の記名押印		
X-1-1	氏名(姓名)	平木 祐輔	

受理官庁記入欄

10-1	国際出願として提出された書類の実際の受理の日	25.12.01
10-2	図面:	
10-2-1	受理された	
10-2-2	不足図面がある	
10-3	国際出願として提出された書類を補完する書類又は図面であってその後期間内に提出されたものの実際の受理の日（訂正日）	
10-4	特許協力条約第11条(2)に基づく必要な補完の期間内の受理の日	
10-5	出願人により特定された国際調査機関	ISA/JP
10-6	調査手数料未払いにつき、国際調査機関に調査用写しを送付していない	

国際事務局記入欄

11-1	記録原本の受理の日	
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PCT手数料計算用紙(願書付属書)

PH-1456-PCT

原本(出願用) - 印刷日時 2001年12月25日 (25. 12. 2001) 火曜日 14時36分25秒

[この用紙は、国際出願の一部を構成せず、国際出願の用紙の枚数に算入しない]

0	受理官庁記入欄			
0-1	国際出願番号.			
0-2	受理官庁の日付印			
0-4	様式-PCT/RO/101 (付属書)			
0-4-1	このPCT手数料計算用紙は、 右記によって作成された。	PCT-EASY Version 2.92 (updated 01. 03. 2001)		
0-9	出願人又は代理人の書類記号	PH-1456-PCT		
2	出願人	旭化成株式会社		
12	所定の手数料の計算	金額/係数	小計 (JPY)	
12-1	送付手数料 T	⇒	18, 000	
12-2	調査手数料 S	⇒	72, 000	
12-3	国際手数料			
	国際出願に含まれる用紙の枚数 (明細書の配列表を除く)	[102]		
	基本手数料 (最初の30枚まで) b1	46, 200		
12-4	30枚を越える用紙の枚数	[72] 807		
12-5	用紙1枚の手数料 (X)	1, 100		
12-6	合計の手数料 b2	[79, 200]	887, 700	
12-4a	追加的部分	400		
12-5b	用紙1枚の手数料 (X)	1, 100		
12-6c	合計の手数料 (添付分 b3)	440, 000		
12-7	b1 + b2 + b3 = B	[565, 400]	933, 900	
12-8	指定手数料 国際出願に含まれる指定国 数	90		
12-9	支払うべき指定手数料の数 (上限は6)	6		
12-10	1指定当たりの手数料 (X)	10, 000		
12-11	合計の指定手数料 D	60, 000		
12-12	PCT-EASYによる料金の減 額 R	-14, 000		
12-13	国際手数料の合計 (B+D-R) I	⇒	979, 900 [611, 400]	
12-14	優先権証明書請求手数料			
	優先権証明書を請求した数	3		
12-15	1優先権証明書当たり (X) の手数料	1, 400		
12-16	優先権証明書請求手数料の 合計 P	⇒	4, 200	
12-17	納付するべき手数料の合計 (T+S+I+P)	⇒	1,074, 100 [705, 600]	
12-19	支払方法	送付手数料: 特許印紙 調査手数料: 特許印紙 国際手数料: 銀行口座への振込み 優先権証明書請求手数料: 特許印紙		

EASYによるチェック結果と出願人による言及

13-1-1	出願人による言及	9109 弁理士 平木祐輔
13-2-3	EASYによるチェック結果 氏名(名称)	Green? 出願人 1: ファクシミリ番号が記入されていません。
13-2-7	EASYによるチェック結果 内訳	Green? 要約書とともに提示する図の番号が示されていません。
		Green? 添付書類“包括委任状の写し”の包括委任状番号が記入されていません。
13-2-8	EASYによるチェック結果 手数料	Green? 使用されている料金表が最新のものであるかどうか、確認してください。
13-2-10	EASYによるチェック結果 注釈	Green? 願書に表示しなければならない通常の項目はすべて他のPCT-EASYの機能で入力することができます。言及を用いた表示の有効性について確認してください。
13-2-11	EASYによるチェック結果 受理官庁/国際事務局記入欄	Green? この願書を作成したPCT-EASYは英語版ないし西欧言語版以外のWindows上で動作しています。ASCII文字以外の文字について、願書と電子データを注意して比較してください。

陳述書

特許庁長官 及川 耕造 殿

本書に添付したフレキシブルディスクに記録した塩基配列またはアミノ酸配列は、明細書に記載した塩基配列またはアミノ酸配列を忠実にコード化したものであって、内容を変更したものでないことを陳述します。

平成 1 3 年 1 2 月 2 5 日

国際出願の表示 2 5 . 1 2 . 0 1 提出の国際出願

発明の名称 NF- κ B活性化遺伝子

出願人（代理人）

氏 名 (9 1 0 9) 弁理士 平 木 祐 輔
HIRAKI Yusuke



あて名 〒105-0001 日本国東京都港区虎ノ門1丁目17番1号
虎ノ門5森ビル 3階

Toranomon No.5 Mori Building Third Floor, 17-1,
Toranomon 1-chome, Minato-ku, Tokyo 105-0001 Japan

フレキシブルディスクの記録形式等の情報を記載した書面

1. 出願人氏名 (名称) 旭化成株式会社
ASAHI KASEI KABUSHIKI KAISHA
2. 代理人氏名 (名称) (9109) 弁理士 平木 祐輔
HIRAKI Yusuke
3. 国際出願の表示 25.12.01 提出の国際出願
4. 発明の名称 NF- κ B 活性化遺伝子
5. 使用した文字コード テキスト形式
6. 配列を記録したファイル名 配列表 (PH-1456-PCT).TXT
7. 連絡先
 - ・電話番号 03 (3503) 8637
 - ・担当者氏名 平木 祐輔



明 細 書

NF- κ B 活性化遺伝子

技術分野

本発明は、NF- κ Bを活性化する作用を有するタンパク質、該タンパク質をコードするDNA、該DNAの取得方法、該DNAを含有する組換えベクター、該組換えベクターを含有する形質転換体ならびに該タンパク質と特異的に反応する抗体に関する。また、本発明は、NF- κ Bの過剰な活性化または阻害が関与する疾患の診断、治療または予防を行う際の本発明のタンパク質、DNAまたは抗体の使用に関する。

また本発明は、該タンパク質、DNA、組換えベクターおよび形質転換体を用いて、NF- κ Bの活性化を阻害または促進する物質をスクリーニングする方法に関する。

背景技術

転写因子NF- κ B (N u c l e a r f a c t o r k a p p a B) は、炎症や免疫反応に関与する種々の遺伝子の転写調節において重要な役割を果たしている。NF- κ Bは、Relファミリーに属するタンパク質のホモあるいはヘテロ二量体からなり、無刺激の状態では、制御タンパク質であるI κ B (I n h i b i t o r o f N F - κ B) と複合体を形成することによりその核移行シグナルが覆い隠され、細胞質内で不活性型として存在する。

細胞にインターロイキン (I L) - 1、腫瘍壊死因子 (T N F) - α などのサイトカインの刺激が与えられると、I κ BはIKK (I κ B k i n a s e) によってリン酸化され、ユビキチン化を経て26Sプロテアソームにより分解される。これにより遊離されたNF- κ Bは核内に移行し、NF- κ B結合配列と呼ばれているDNA配列に結合し、その制御下の遺伝子の転写を誘導する。NF- κ Bによって発現調節を受けているとされている遺伝子は免疫グロブリン遺伝子の他、I L - 1、T N F - α などの炎症性サイトカイン、インターフェロン、細

胞接着因子等が知られており、NF- κ Bはこれらの遺伝子の発現誘導を介して、炎症や免疫応答に関わっている。

NF- κ Bの機能あるいは活性化を阻害することによって、炎症・免疫疾患やその他の疾病、たとえば腫瘍増殖、に関与している多くの因子（タンパク質）の発現を抑制できる可能性があり、自己免疫や炎症を原因・症状とする疾病に対する医薬の有望な標的である〔たとえば、*Clinical Chemistry* 45, 7-17 (1999)、*J. Clin. Pharmacol.* 38, 981-993 (1998)、*Gut* 43, 856-860 (1998)、*The New England Journal of Medicine* 366, 1066-1071 (1997)、*TIPS* 46-50 (1997)、*The FASEB Journal* 9, 899-909 (1995)、*Nature* 395, 225-226 (1998)、*Science* 278, 818-819 (1997)、*Cell* 91, 299-302 (1997)〕。

細胞外からの情報は、何らかのシグナルの形に変えて、細胞膜を通過し細胞質をこえて核に到達し、標的遺伝子の発現を調節して細胞の応答が引き起こされる。そのため、細胞外の刺激からNF- κ Bの活性化に至る細胞内におけるシグナル伝達の仕組みを解明することは、自己免疫疾患や炎症症状を呈する疾患に対する新たな医薬の開発あるいは治療法の開発に非常に重要な手段を提供することとなり、極めて重要な意義を有している。

しかしながら、細胞が一定の刺激を受けてからNF- κ Bの活性化に至るまでのシグナル伝達経路にはプロテインキナーゼなどの各種伝達分子に関わる多くのステップの存在が考えられ、従って、より効率的な創薬研究のためには、主要な役割を果たす伝達分子を明らかにした上でそれらに焦点をしばった新しい薬物スクリーニング方法を確立することが望まれる。しかし、NF- κ Bの活性化のメカニズムは上記IKK、ユビキチン化酵素、26Sプロテアソームの他、TNF receptor associated factor 2 (TRAF2) や NF- κ B inducing kinase (NIK) などの幾つかのシグナル伝達分子が同定され、少しずつ解明されつつあるものの、いまだ不明な点が多く、新たなシグナル伝達分子の同定とより進んだNF- κ B活性化メカニズムの

解明が望まれていた。

発明の開示

本発明の課題は、上記のように有用なNF- κ Bを直接的、あるいは間接的に活性化する作用を有する新規な遺伝子、タンパク質を見出し、これを医薬、診断薬、医療の分野で利用する方法を提供することにある。即ち、NF- κ Bを活性化作用を有する新規タンパク質、該タンパク質をコードするDNA、該DNAを含有する組換えベクター、該組換えベクターを含有する形質転換体、該タンパク質の製造方法、該タンパク質またはその部分ペプチドに対する抗体、該抗体の製造方法を提供する。

また、本発明は、該タンパク質、DNA、組換えベクターおよび形質転換体を用いて、NF- κ Bの活性化を阻害または促進する物質をスクリーニングする方法、該スクリーニング用キット、該スクリーニング方法もしくはスクリーニング用キットを用いて得られるNF- κ Bの活性化を阻害または促進する物質、該物質の製造方法、NF- κ Bの活性化を阻害または促進する物質を含有している医薬などを提供する。

近年、生体内で発現している遺伝子を解析する手段として、cDNAの配列をランダムに解析する研究が活発に行われており、このようにして得られたcDNAの断片配列がEST (Expressed Sequence Tag、たとえば <http://www.ncbi.nlm.nih.gov/dbEST>) として、データベースに登録され公開されている。しかし、ESTは配列情報のみであり、その機能を推定することは困難である。また、ESTはUniGene (<http://www.ncbi.nlm.nih.gov/UniGene>) により整備され、これまでに約92000クラスターに登録されている。しかし、その多くは5'端ヌクレオチド配列を欠損しており、タンパク質翻訳開始部位を含まない。そのため、mRNAのコード領域の決定を前提とするタンパク質の機能解析、プロモーターの解析による遺伝子発現制御の理解といった遺伝子機能の解析に直結しているとはいいがたい。

一方、遺伝子の産物、すなわちタンパク質の機能を解明する方法の一つに、動物細胞を用いた一過性発現クローニング法がある (たとえば、実験医学別冊 遺

伝子工学ハンドブック)。この方法は、動物細胞発現ベクターを用いて作製した cDNA ライブラリーを、動物細胞にトランスフェクションすることで機能的なタンパク質を直接発現させ、このタンパク質が細胞に及ぼす生物活性を指標として cDNA を同定、クローニングする方法である。この方法では、目的とするタンパク質産物に関する化学的情報（アミノ酸配列や分子量）をあらかじめ必要とせず、細胞内や培養液中に発現しているタンパク質の特異的生物活性を検出して cDNA クローンの同定を行うことができる。

この発現クローニングを効率良く行なうためには、cDNA ライブラリーの作製方法を工夫する必要がある。なぜなら、従来より汎用されている cDNA ライブラリー作製方法には幾つかの方法があるが（たとえば Gubbl er-Hoffman の方法: Gene 25 (1983) オカヤマ-バーグの方法: Mol. Cell. Biol. 2 (1982)), これらの方法によって作製された cDNA は、そのほとんどが 5' 末端ヌクレオチド配列を欠損したものであり、完全長（mRNA の全ヌクレオチド配列を含む）であることは稀であるからである。その理由は、mRNA から cDNA を作るのに使用する逆転写酵素が、完全長の cDNA を作る効率が必ずしも高くないからである。

さらに、遺伝子の機能解析を試みるに際しては、完全長 cDNA をクローニングし、そこからタンパク質を発現させることが必須の要件である。従って、全体のクローンの中で、完全長のものの割合が高いライブラリーを作製することが、発現クローニングを効率良く行なうために必要であった。

本発明者らは、上記課題を解決するために鋭意研究を重ねた結果、オリゴキャッピング法を用いて完全長 cDNA ライブラリーを作製し、293-EBNA 細胞を用いた発現クローニング法による遺伝子機能アッセイ系を完成し、該アッセイ系により NF- κ B を活性化する作用を有するタンパク質をコードする新規 DNA (cDNA) を単離することに成功した。この新規 DNA は、293-EBNA 細胞内で発現させることにより NF- κ B の活性化を誘発した。この結果は、この新規 DNA が NF- κ B の活性化に関与するシグナル伝達分子であることを示しており、本発明を完成するに至った。

すなわち、本発明は

(1) 以下の(a)または(b)の精製されたタンパク質。

(a) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質。

(b) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかにおいて1若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつNF- κ Bを活性化する作用を有するタンパク質。

(2) 上記(1)記載のタンパク質とその全長にわたり少なくとも95%のアミノ酸配列の同一性を有するタンパク質であり、かつNF- κ Bを活性化する作用を有する、精製されたタンパク質。

(3) 以下の(a)または(b)のタンパク質をコードするヌクレオチド配列を包含する、単離されたポリヌクレオチド。

(a) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、4

7、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質。

(b) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかにおいて1若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつNF- κ Bを活性化する作用を有するタンパク質。

(4) 以下の(a)～(c)のいずれかのポリヌクレオチド配列を含む単離されたポリヌクレオチド。

(a) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、16

7、169、171、173、175、177または179のいずれかで表されるポリヌクレオチド配列。

(b) (a)のポリヌクレオチド配列と相補的なポリヌクレオチド配列を有するポリヌクレオチドとストリンジェントな条件下でハイブリダイズし、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

(c) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかにおいて、1若しくは複数個のヌクレオチド配列が欠失、置換若しくは付加されたポリヌクレオチド配列からなり、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

(5) 上記(3)記載のポリヌクレオチドと全長にわたり少なくとも95%以上の同一性を有し、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

(6) 上記(4)記載のポリヌクレオチドと全長にわたり少なくとも95%以上の同一性を有し、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

(7) 上記(3)～(6)のいずれか1つに記載のポリヌクレオチドによりコードされる精製されたタンパク質。

(8) 上記(3)～(6)のいずれか1つに記載のポリヌクレオチドを含有する組換えベクター。

(9) 上記(8)に記載の組換えベクターを含む形質転換された細胞。

(10) 上記(1)または(2)に記載のタンパク質が膜タンパク質である場

合における、上記（９）記載の細胞の膜。

（１１） （a）上記（３）～（６）のいずれか１つに記載の単離されたポリヌクレオチドがコードするタンパク質を発現する条件下で該ポリヌクレオチドを含有する形質転換された細胞を培養し、

（b）培養物からタンパク質を回収する、
ことを含む、タンパク質の製造方法。

（１２） （a）個体のゲノムにおける上記（１）、（２）または（７）に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、
および／または

（b）該個体に由来するサンプル中での該タンパク質の発現量を分析する、
ことを含む該個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法。

上記方法において、好ましくは、発現するタンパク質の量が正常の２倍以上の場合、あるいは２分の１以下の場合に病気であると診断する。

（１３） 以下の工程を含むNF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングする方法。

（a）NF- κ Bを活性化するタンパク質をコードする遺伝子およびNF- κ Bの活性化に対応した、検出可能シグナルを提供しうる成分を細胞に提供する工程、

（b）該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された細胞を培養する工程、

（c）該形質転換された細胞と１あるいは複数個の候補化合物とを接触させる工程、

（d）検出可能なシグナルを測定する工程、および

（e）該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物として単離もしくは同定する工程。

また、シグナルを正常より２倍以上増加させる化合物を活性化剤化合物として単離または同定し、２分の１以下に減少させる化合物を阻害剤化合物として単離または同定することが好ましい。

（１４） 以下の工程を含む、医薬組成物を製造する方法。

(a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子、および検出可能なシグナルを提供しうる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された宿主細胞を培養する工程、

(c) 該形質転換された宿主細胞と1あるいは複数個の候補化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、

(e) 該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物を単離もしくは同定する工程、および

(f) 単離または同定された化合物を医薬組成物として最適化する工程。

また、本発明においては、シグナルを正常より2倍以上増加させる化合物を活性化剤化合物として単離または同定し、2分の1以下に減少させる化合物を阻害剤化合物として単離または同定することが好ましい。

(15) NF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットであって、

(a) NF- κ Bを活性化するタンパク質をコードする遺伝子、およびNF- κ Bの活性化後、検出可能なシグナルを提供しうる成分により形質転換された細胞、および

(b) 検出可能なシグナルを測定するための試薬を含むキット。

(16) 上記(1)、(2)または(7)に記載のタンパク質に特異的に結合するモノクローナルあるいはポリクローナル抗体。

(17) 上記(1)、(2)または(7)に記載のタンパク質を抗原あるいはエピトープ含有フラグメントとして非ヒト動物に投与することからなる、上記(1)、(2)または(7)に記載のタンパク質に特異的に結合するモノクローナルまたはポリクローナル抗体の製造方法。

(18) NF- κ Bの活性化タンパク質の発現を阻害する、上記(3)～(6)のいずれか1つに記載のポリヌクレオチドに相補的なアンチセンスオリゴヌクレオチド。

(19) 上記(1)、(2)または(7)記載のタンパク質をコードするRNAの開裂により、NF- κ Bの活性化を阻害するリボザイム。

(20) 炎症、自己免疫疾患、感染症、癌および骨疾患からなる群から選択される疾患の治療に有効な量の上記(13)記載の方法でスクリーニングされた化合物および／または上記(16)記載のモノクローナルまたはポリクローナル抗体および／または上記(18)記載のアンチセンスオリゴヌクレオチドおよび／または上記(19)記載のリボザイムを個体に投与することを含む疾患の治療法。

(21) NF- κ Bの活性化を阻害または活性化するものとして上記(14)に記載の方法により製造された医薬組成物。

(22) 炎症、自己免疫疾患、癌、感染症、骨疾患、AIDS、神経変性疾患、または虚血性障害の治療のための上記(21)記載の医薬組成物。

(23) NF- κ Bに関連する疾患を患っている患者に上記(14)記載の方法により製造された医薬組成物を投与することからなる炎症、自己免疫疾患、癌疾患、感染症、骨疾患、AIDS、神経変性疾患、または虚血性障害を治療する方法。

(24) 上記(16)記載のモノクローナルまたはポリクローナル抗体を有効成分として含有する医薬組成物。

(25) 上記(18)記載のアンチセンスオリゴヌクレオチドを有効成分として含有する医薬組成物。

(26) 対象疾患が炎症、自己免疫疾患、感染症、癌疾患、骨疾患、AIDS、神経変性疾患および虚血性障害からなる群から選択される、上記(24)または(25)に記載の医薬組成物。

(27) 機能を有する新規遺伝子の取得方法であり、少なくとも以下の工程を含む方法。

- (a) オリゴキャッピング法を用いて完全長cDNAライブラリーを作製し、
- (b) 完全長cDNAおよび該機能を有するタンパク質の存在を示すシグナルを発する因子を含有するプラスミドを細胞中にコトランスフェクションし、さらに
- (c) シグナルを発するプラスミドを選択する。

尚、本発明における機能を有する新規遺伝子とは、例えば生物活性を持つタン

パク質をコードする核酸分子が挙げられる。

(28) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177および179で表されるヌクレオチド配列のうち少なくとも1以上を含むデータセットおよび／または配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178および180で表されるアミノ酸配列のうち少なくとも1以上を含むデータセットを保存したコンピュータ読み込み可能媒体。

(29) 上記(28)に記載の媒体上のデータと他のヌクレオチド配列および／または他のアミノ酸配列のデータを比較して他のポリヌクレオチド配列および／またはアミノ酸配列との同一性の算出を行う方法。

(30) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、11



4、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179から選択されるヌクレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質。

(31) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質。

本明細書は本願の優先権の基礎である日本国特許出願 2000-402288 号、2001-088912 号及び 2001-254018 号、並びに、米国仮出願 60/258,315 号、60/278,640 号及び 60/314,385 号の明細書及び／または図面に記載される内容を包含する。

図面の簡単な説明

図1は、実施例3配列番号5のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。図中で横軸は、MG-132濃度、縦軸は、MG-132無添加(0 μ M)条件での相対ルシフェラーゼ活性値を100%とした相対値を示す(各濃度での相対ルシフェラーゼ活性値をMG-132無添加条件での相対ルシフェラーゼ活性で割ってパーセント表示した)。

図 2 は、実施例 3 配列番号 9 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 3 は、実施例 3 配列番号 17 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 4 は、実施例 3 配列番号 21 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 5 は、実施例 3 配列番号 35 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 6 は、実施例 3 配列番号 37 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 7 は、実施例 3 配列番号 41 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 8 は、実施例 3 配列番号 53 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 9 は、実施例 3 配列番号 57 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 10 は、実施例 3 配列番号 63 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 11 は、実施例 3 配列番号 67 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 12 は、実施例 3 配列番号 71 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 13 は、実施例 3 配列番号 75 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 14 は、実施例 3 配列番号 81 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 15 は、実施例 3 配列番号 87 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 16 は、実施例 3 配列番号 91 のプロテアソーム阻害剤 MG-132 による

NF- κ Bのレポーター活性抑制を示す図である。

図17は、実施例3配列番号93のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図18は、実施例3配列番号97のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図19は、実施例3配列番号121のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図20は、実施例3配列番号123のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図21は、実施例3配列番号129のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図22は、実施例3配列番号154のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図23は、実施例3配列番号158のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図24は、実施例3配列番号162のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図25は、実施例3配列番号168のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図26は、実施例3配列番号170のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図27は、実施例3配列番号172のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図28は、実施例3配列番号176のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図29は、実施例3配列番号178のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

配列表の説明

配列番号 181 はプライマーである。

配列番号 182 はプライマーである。

発明を実施するための形態

まず、本発明の基本的特徴を更に明らかにするために、本発明の完成に至る経緯を追いながら、本発明について説明する。NF- κ B を活性化する作用を有する新規遺伝子を取得する目的で、実施例に示すように、以下の実験を実行した。まずヒト正常肺線維芽細胞（三光純薬株式会社より購入）より調製した mRNA より、オリゴキャッピング法によって完全長 cDNA を作製し、該 cDNA をベクター pME18S-FL3（GenBank Accession AB009864）に組み込んだ完全長 cDNA ライブラリーを作製した。次に、該 cDNA ライブラリーを大腸菌に導入し、1 クローンずつプラスミドを調製した。次に、293-EBNA 細胞（インビトロジェン社）に、ルシフェラーゼをコードする DNA を含有する pNF κ B-Luc レポータープラスミド（STRATAGENE 社）と上記の完全長 cDNA プラスミドとを共導入した。そして、24 時間あるいは 48 時間培養後、ルシフェラーゼ活性を測定し、ルシフェラーゼ活性が対照実験（完全長 cDNA の代わりに、ベクター pME18S-FL3 を入れた細胞）と比べて有意に上昇している（対照実験と比べてルシフェラーゼ活性が 5 倍以上の値を示した）プラスミドを選抜し、該プラスミドにクローニングされている cDNA の全ヌクレオチド配列を決定した。このようにして得られた cDNA によりコードされるタンパク質は、該タンパク質が NF- κ B の活性化に関与するシグナル伝達分子であることを示している。

次に、以下に本発明について詳細に説明する。

本発明における NF- κ B を活性化する作用を有するとは、適切な細胞内に遺伝子を導入し、該遺伝子にコードさせるタンパク質を過剰発現させた時、NF- κ B が直接的あるいは間接的に活性化される（NF- κ B の活性化を誘発する）ことをいう。NF- κ B の活性化は、例えば、NF- κ B 依存レポーター遺伝子を用いたアッセイにより測定できる。アッセイは、該レポーター活性を対照細胞（ベクターのみを導入した細胞）に比し上昇させる作用を有することをいう。レ

ポーター活性の上昇は、好ましくは、1.5倍以上、さらに好ましくは、2倍以上、さらに好ましくは5倍以上である。

レポーター活性は、発現させたいタンパク質をコードするポリヌクレオチド(例えばcDNA)を適切な発現ベクター内にクローニングし、該発現ベクターとNF- κ B依存レポータープラスミドを適切な細胞に共導入(コ・トランスフェクション)し、一定時間培養後、レポーターの活性を測定することにより測定することができる。適切な発現ベクターは当業者にはよく知られており、例えば、pME18S-FL3、pcDNA3.1(Invitrogen社)などが挙げられる。レポーター遺伝子は、当業者がその発現を容易に検出できるものであればよく、例えば、ルシフェラーゼ、クロラムフェニコールアセチルトランスフェラーゼ、 β -ガラクトシダーゼをコードする遺伝子である。ルシフェラーゼをコードする遺伝子を使用することが最も好ましく、NF- κ B依存レポータープラスミドとしては、例えば、pNF- κ B-Luc(STRATAGENE社)が例示される。適切な細胞とは、IL-1あるいはTNF- α などの刺激によりNF- κ Bが活性化される応答を示すような細胞であり、例えば、293-EBNA細胞が挙げられる。細胞培養および細胞への遺伝子導入(トランスフェクション)は、当業者であれば当該技術分野で公知の慣用方法により実施でき最適化できる。

好ましい方法としては、293-EBNA細胞を細胞培養用96穴プレートに 1×10^4 cells/wellの細胞数となるように、5%FBS(Fetal Bovine Serum)存在下のDMEM(Dulbecco's Modified Eagle Medium)培地にまき、5%CO₂存在下、37℃で24時間培養した後、FuGENE6(Roche社)を用いて、pNF- κ B-Lucレポータープラスミド(STRATAGENE社)と、発現ベクターを1ウェルに共導入する。37℃で24時間培養後、ロングタームルシフェラーゼアッセイシステムピッカジーンLT2.0(東洋インキ社)を用いて、ルシフェラーゼ活性を測定することによりNF- κ Bの活性化を測定する。ルシフェラーゼ活性の測定は、例えば、PerkinElmer社のWallac ARVOTMST 1420 MULTILABEL COUNTERを用いて測定できる。FuGENE6による遺伝子導入の方法及びピッカ

ジーンLT2.0によるルシフェラーゼ活性測定は、それぞれに添付されているプロトコールに従い実施できる。FuGENE 6を用いた96穴プレートでの遺伝子導入の方法は、1ウエルあたり、FuGENE 6の量は0.3~0.5 μ lが良く、好ましくは0.3 μ lであり、pNF- κ B-Lucプラスミドの量は50~100 ngが良く、好ましくは50 ngであり、発現ベクターの量は、50~100 ngが良く、好ましくは100 ngである。NF- κ Bを活性化する作用を有するとは、該レポーター活性（ルシフェラーゼ活性）を対照実験（空のベクターのみを導入した細胞）に比し、上昇させる作用を有することをいう。レポーター活性の上昇は、好ましくは1.5倍以上、さらに好ましくは、2倍以上、さらに好ましくは5倍以上である。

配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかのアミノ酸配列に関連して、本発明は、以下のタンパク質を提供する。

(a) 上記アミノ酸配列を含むタンパク質。
(b) 上記アミノ酸配列の1つを有するペプチド。
(c) NF- κ Bを活性化し、かつ上記アミノ酸配列において、1以上のアミノ酸の削除、置換または付加を有するタンパク質。

(d) その全長にわたり配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、1

11、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のアミノ酸配列に少なくとも95%、好ましくは97~99%の同一性を有するアミノ酸配列を含むタンパク質。

“同一性”とは、当該技術で知られているとおり、配列を比較することにより決定される、2以上のタンパク質あるいは2以上のポリヌクレオチドの間の関係である。当該技術で“同一性”とは、タンパク質またはポリヌクレオチド配列の間の適合によって、あるいは場合によっては、一続きのそのような配列間の適合によって決定されるような、タンパク質またはポリヌクレオチド配列の間の配列相関性の程度を意味する。“同一性”および“類似性”は、既知の方法により容易に決定できる。同一性を決定する好ましい方法は、試験する配列間で最も長く適合するように設計される。同一性および類似性を決定するための方法は、公に利用可能なプログラムにコードされている。相同性決定には、Altschul らによる BLAST (Basic Local Alignment Search Tool) プログラム (たとえば、Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ., J. Mol. Biol., 215: p403-410 (1990), Altschul SF, Madden TL, Schaffer AA, Zhang J, Miller W, Lipman DJ., Nucleic Acids Res. 25: p3389-3402 (1997)) を利用し決定することができる。BLAST のようなソフトウェアを用いる場合、デフォルト値を用いるのが好ましい。BLAST 検索に一般的に用いられる主な初期条件は、以下の通りであるが、これに限定されない。

アミノ酸置換行列とは20種類のアミノ酸の各々のペアの類縁性を数値化した行列であり、通常 BLOSUM62 のデフォルトマトリックスが用いられる。このアミノ酸置換行列の理論については Altschul S. F., J. Mol. Biol., 219:555-565 (1991) に、DNA 配列の比較への適用については States D. J., Gish W., Altschul S. F., Methods, 3:66-70 (1991) に示されている。その際の最適なギャップコストは経験的に決定されており、BLOSUM62 の場合は好ましくは、Existence 11、Extension 1 のパラメーターが用いられる。期待値 (EXPECT) とは、データベース配列に対し

てマッチする際の統計的有意性に関する閾値であり、デフォルト値は10である。

一例として、配列番号2のアミノ酸配列に対して例えば95%以上の同一性を有するタンパク質は、そのアミノ酸配列が配列番号2のアミノ酸配列のアミノ酸100個あたり5個までのアミノ酸の変化を含んでよいことを意味する。言い換えれば、対照アミノ酸配列に対して95%以上のアミノ酸配列の同一性を有するタンパク質は、対照配列中の全アミノ酸の5%までの数のアミノ酸が欠失または他のアミノ酸と置換していてもよく、あるいは、対照配列中の全アミノ酸配列のうち5%までの数のアミノ酸が対照配列中に挿入されたものであっても良い。対照配列におけるこれらの変化は、対照アミノ酸配列のアミノ末端またはカルボキシ末端位置に存在していてもよく、あるいはそれらの末端間のいずれかの位置に存在していてもよく、あるいは対照配列内で1個またはそれ以上の一連の群をなしていてもよい。

上記した配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかに記載されたアミノ酸配列からなるタンパク質がNF- κ Bを活性化する作用を有することは、本願明細書実施例に記載の通りである。

配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、1

34、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかのポリヌクレオチドに関連して、本発明は、また以下の単離されたポリヌクレオチドを提供する。

(a) 上記配列に少なくとも95%、好ましくは97-99%の同一性を有するヌクレオチド配列を含むポリヌクレオチド。

(b) 上記配列のポリヌクレオチド。

(c) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかのアミノ酸配列に少なくとも95%、好ましくは97-99%の同一性を有するアミノ酸配列を有するタンパク質をコードするヌクレオチド配列を有するポリヌクレオチド。

上記ヌクレオチド配列に含まれるヌクレオチド配列に同一またはほとんど同一なポリヌクレオチドは、本発明のタンパク質をコードする全長cDNA及びゲノムクローンまたは上記配列に対応する相同性の高い他の遺伝子のcDNAまたはゲノムクローンを単離するためのハイブリダイゼーションプローブとして、または核酸増幅反応のためのプライマーとして使用してもよい。代表的には、これらのヌクレオチド配列は、上記配列に70%同一であり、好ましくは、80%同一であり、より好ましくは90%同一であり、最も好ましくは、95%同一である。プローブまたはプライマーは、一般的には少なくとも15ヌクレオチドを含有し、好ましくは30ヌクレオチドを含有し、50ヌクレオチドを含有してもよい。特に好ましいプローブは、30-50ヌクレオチドを有する。特に好ましいプライマーは、20-25ヌクレオチドを有する。

本発明のポリヌクレオチドは、DNAの形態(たとえば、cDNAおよびクローニングによって得られるか、あるいは合成的に生成されるゲノムDNAを含む)であってもよく、RNA(たとえばmRNA)の形態であってもよい。該ポリヌクレオチドは、二本鎖であっても、一本鎖であってもよい。二本鎖の場合は、二本鎖DNA、二本鎖RNAまたはDNA:RNAのハイブリッドであってもよい。一本鎖の場合は、センス鎖(コード鎖としても知られる)であっても、アンチセンス鎖(非コード鎖としても知られる)であってもよい。

当業者であれば、公知の方法を用いてこのタンパク質中のアミノ酸の置換などを適宜行い、配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかに記載のアミノ酸配列を有するタンパク質と同様にNF- κ Bを活性化する作用を有するタンパク質を作製することが可能である。一つの方法としては、該タンパク質をコードするDNAに対して、慣用の突然変異誘発法を使用する方法がある。別の方法としてはたとえば部位特異的変異法(たとえば宝酒造株式会社のMutagen-Super Express Kmキット)が挙げられる。また、タンパク質のアミノ酸の変異は自然界においても生じうる。このようにアミノ酸の欠失、置換、付加により配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、

131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかのタンパク質に対してアミノ酸配列が変異した変異体であって、NF- κ Bを活性化作用を有するタンパク質及び該タンパク質をコードするDNAも本発明に含まれる。変異の数は、好ましくは10まで、より好ましくは5まで、最も好ましくは3までが好ましい。

アミノ酸置換の例としては、保存的置換が好ましく、具体的には以下のグループ内での置換が挙げられる。(グリシン、アラニン)(バリン、イソロイシン、ロイシン)(アスパラギン酸、グルタミン酸)(アスパラギン、グルタミン)(セリン、トレオニン)(リジン、アルギニン)(フェニルアラニン、チロシン)。

当業者であれば、ハイブリダイゼーション技術などを用いて配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質をコードするDNA(たとえば配列番号2)またはその一部を基に、これと類似性の高いDNAを単離して、該DNAから配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、14

1、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180で表されるアミノ酸配列からなるタンパク質と同様に NF- κ B を活性化する作用を有するタンパク質を得ることも通常行い得ることである。このように上記した配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列のタンパク質と高い同一性を有するタンパク質であって、NF- κ Bを活性化する作用を有するタンパク質も本発明のタンパク質に含まれる。高い同一性とは、上記配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかであらわされるアミノ酸配列の全長にわたり少なくとも90%、好ましくは95%、さらに好ましくは、少なくとも97以上の同一性を有するアミノ酸配列を示す。

本発明のタンパク質としては、ヒトや哺乳動物のあらゆる細胞や組織に由来する天然のタンパク質でもよく、化学合成タンパク質であってもよく、また遺伝子

組換え技術によって得られたタンパク質でもよい。タンパク質は糖鎖やリン酸化などの翻訳後修飾は受けていても受けていなくても良い。

本発明は、上記で示される本発明のタンパク質をコードするポリヌクレオチドである。上記の配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質をコードするヌクレオチド配列としてより具体的には、たとえば配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかで表されるヌクレオチド配列が挙げられる。DNAはcDNAのほか、ゲノムDNA、化学合成DNAも含まれる。遺伝暗号の縮重に従い、遺伝子から生産されるタンパク質のアミノ酸配列を変えずに配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、

105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質をコードするヌクレオチド配列の少なくとも1つのヌクレオチドを他の種類のヌクレオチドに置換することができる。従って、本発明のDNAはまた、遺伝暗号の縮重に基づく置換によって変換されたヌクレオチド配列も含有する。このようなDNAは、公知の方法により合成することができる。

本発明のDNAは、配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかで表されるヌクレオチド配列からなるDNAとストリンジェントな条件下でハイブリダイズし、かつNF- κ Bを活性化する作用を有するタンパク質をコードするDNAも含まれる。ストリンジェントな条件とは、当業者には十分理解できることであり、たとえば、T. Maniatisらの実験操作書（Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory 1982、1989）に従えば容易に実施できる。

すなわち、ストリンジェントな条件とは、30%ホルムアミドを含むハイブリダイゼーション溶液中（5×SSC（0.75MのNaCl、75mMのクエン酸三ナトリウム）、5×デンハルト溶液、0.5%SDS、100 μ g/mlの変性せん断サケ精子DNA）で37℃のインキュベーションを一晩行い、その後2

×SSC、0.1%SDS中、室温で10分の洗浄を3回行い、次いで1×SSC、0.1%SDS中、37℃で10分の洗浄を2回行う条件である（低ストリンジエンシー）。より好ましい条件は、40%ホルムアミドを含むハイブリダイゼーション溶液中で42℃のインキュベーションを一晩行い、その後2×SSC、0.1%SDS中、室温で10分の洗浄を3回行い、次いで0.2×SSC、1%SDS中、42℃で10分の洗浄を2回行う条件である（中ストリンジエンシー）。最も好ましい条件は、50%ホルムアミドを含むハイブリダイゼーション溶液中で42℃のインキュベーションを一晩行い、その後2×SSC、0.1%SDS中、室温で10分の洗浄を3回行い、次いで0.2×SSC、0.1%SDS中、50℃で10分の洗浄を2回行う条件である（高ストリンジエンシー）。この際、得られたDNAは、NF- κ Bを活性化する作用を有するタンパク質をコードすることが必須である。

本発明は、上記（3）あるいは（4）のポリヌクレオチドのヌクレオチド配列と高い類似性を有し、かつNF- κ Bを活性化する作用を有するタンパク質をコードするヌクレオチドを含むポリヌクレオチドを含む。代表的には、これらのヌクレオチド配列は、上記（3）または（4）のポリヌクレオチドのヌクレオチド配列の全長にわたり95%同一であり、より好ましくは97%同一であり、最も好ましくは少なくとも99%同一である。

上記の本発明のDNAは、前述のタンパク質を、組換えDNA技術を用いて製造するのに用いることができる。本発明のDNA及びペプチドは、概略以下のようにして得ることができる。

- (A) 本発明のタンパク質をコードするDNAをクローニングする。
- (B) タンパク質の全コード領域あるいはその一部をコードするDNAを発現用ベクターに組み込んで、組換えベクターを構築する。
- (C) 構築した組換えベクターにより、宿主細胞を形質転換する。
- (D) 得られた細胞を培養し、該タンパク質、またはその類縁体を発現させ、カラムクロマトグラフィーにより精製する。

上記の工程でDNA、組換え体宿主としての大腸菌等の取り扱いに必要な一般的な操作は、当業者間で通常行われているものであり、たとえば、上記T. M

a n i a t i sらの実験操作書に従えば容易に実施できる。使用する酵素、試薬類も全て市販の製品を用いることができ、特に断らない限り、製品で指定されている使用条件に従えば、完全にそれらの目的を達成することができる。以下に上記（A）～（D）の工程について更に詳しく説明する。

上記（A）における本発明のタンパク質をコードするDNAのクローニングの手段としては、本願明細書実施例に記載した方法の他に、本発明のヌクレオチド配列（たとえば配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれか）の一部を有する合成DNAをプライマーとしたPCR法によって増幅する方法、あるいは、適当なベクターに組み込んだDNAを本発明のタンパク質の一部あるいは全領域をコードするDNA断片もしくは合成DNAを標識したものとのハイブリダイゼーションによって選別すること、などが挙げられる。細胞、組織より全RNAまたはmRNA画分を調製したものを用いて直接Reverse Transcription（RT-PCR法）によって増幅することもできる。適当なベクターに組み込んだDNAとしては、たとえば市販されている（CLONTECH社、STRATAGENE社）ライブラリーを使用することができる。ハイブリダイゼーションの方法は、当業者間で通常行われているものであり、たとえば、上記T. Maniatisらの実験操作書に従えば容易に実施できる。クローン化された本発明のタンパク質をコードするDNAは目的によりそのまま、または所望により制限酵素で消化したり、リンカーを付加したりして使用することができる。上記のようにして得られるDNAは、配列番号2、4、6、8、10、12、14、16、

18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかに記載のヌクレオチド配列を有する遺伝子であるか、あるいは前述の(3)～(6)のポリヌクレオチドであればよい。上記(B)において発現ベクターに組み込むDNAは、上述のタンパク質の全長をコードする全長cDNAでも、DNA断片でも良いし、その一部分を発現する様に構築されたDNA断片でも良い。

すなわち、本発明は、上記のDNAを含有する組換えベクターである。

本発明のタンパク質の発現ベクターは、たとえば、本発明のタンパク質をコードするDNAから目的とするDNA断片を切り出し、該DNA断片を適当な発現ベクター中のプロモーターの下流に連結することにより製造することができる。

用いる発現ベクターとしては、複製可能であれば、大腸菌をはじめとする原核生物由来、酵母由来、真菌由来、昆虫ウイルス由来、脊椎動物ウイルス由来いずれのベクターでも良いが、宿主として使用する微生物または細胞に適したものを選択する必要がある。また、発現物に応じて、宿主細胞－発現ベクター系としては、適切な組み合わせが選択される。

微生物を宿主として使用する場合、これら微生物に適したプラスミドベクターが組み換え体DNAの複製可能な発現ベクターとして一般に用いられる。

たとえば、大腸菌を形質転換するためのプラスミドベクターとしては、プラスミドpBR322やpBR327などを用いることができる。プラスミドベクターは通常複製起源、プロモーター、及び組換え体DNAで形質転換した細胞を選別するのに有用な表現型を組換え体DNAに与えるマーカー遺伝子等を含んでいる。プロモーターの例としては、 β -ラクタマーゼプロモータ、ラクトースプロ

モーター、トリプトファンプロモーター等が挙げられる。マーカー遺伝子の例としては、アンピシリン耐性遺伝子やテトラサイクリン遺伝子などが挙げられる。適した発現ベクターの例としては、プラスミド pBR322、pBR327 の他に、pUC18、pUC19 等が挙げられる。

酵母で本発明の DNA を発現するためには、複製可能なベクターとして、たとえば YEp24 を用いることができる。プラスミド YEp24 は URA3 遺伝子を含っており、この URA3 遺伝子をマーカー遺伝子として利用することができる。酵母細胞用の発現ベクターのプロモーターの例としては、3-ホスホグリセレートキナーゼ、グリセルアルデヒド-3-ホスフェートデヒドロゲナーゼ、アルコールデヒドロゲナーゼなどの遺伝子プロモーター等が挙げられる。

真菌で本発明の DNA を発現するための発現ベクターに用いられるプロモーター及びターミネーターの例としては、ホスホグリセレートキナーゼ (PGK)、グリセルアルデヒド-3-ホスフェートデヒドロゲナーゼ (GAPD)、アクチン等の遺伝子プロモーター及びターミネーターが挙げられる。適した発現ベクターの例としては、プラスミド pPGACY2、pBSFAHY83 等が挙げられる。

昆虫細胞で本発明の DNA を発現させるための発現ベクターに用いられるプロモーターの例としては、ポリヘドリンプロモーター、P10 プロモーターなどが挙げられる。

動物細胞で本発明の DNA を発現させるための組換えベクターは、一般に遺伝子を制御するための機能配列、たとえば、複製起源、本発明の DNA の上流に位置すべきプロモーター、リボソーム結合部位、ポリアデニル化部位や転写終止配列を含んでいる。本発明の DNA を真核細胞内で発現させるのに用いることができるそのような機能配列はウイルスやウイルス性物質から得ることができる。例えば、SR α プロモーター、SV40 プロモーター、LTR プロモーター、CMV (サイトメガロウイルス) プロモーター、HSV-TK プロモーターなどがあげられる。これらのうち、CMV プロモーター、SR α プロモーターなどを用いるのが好ましい。また、本発明のタンパク質をコードする遺伝子の上流位置に本来存在するプロモーターも、上述の宿主-ベクター系で使用するのに適しているならば使用することができる。複製起源については、外来性の起源、たとえばア

デノウイルス、ポリオーマ、SV40等のウイルス由来の複製起点を用いることができる。また、発現ベクターとして宿主染色体に組み込まれるような性質を有するベクターを用いる場合、宿主染色体の複製起源を利用することができる。適した発現ベクターの例としては、プラスミドpSV-dhfr(ATCC 37146)、pBPV-1(9-1)(ATCC 37111)、pcDNA3.1(INVITROGEN社)、pME18S-FL3等が挙げられる。

本発明は、上記の組換えベクターを含む形質転換された細胞である。本発明の複製可能な組換えベクターで形質転換された微生物または細胞は、前述の通り、組換えベクターに与えられた少なくとも1種の表現型によって形質転換されずに残った親細胞から選別される。表現型は少なくとも1種のマーカー遺伝子を組換えベクターに挿入することによって与えることができる。また複製可能なベクターが本来有しているマーカー遺伝子を利用することもできる。マーカー遺伝子の例としては、たとえば、ネオマイシン耐性などの薬剤耐性遺伝子やジヒドロ葉酸レダクターゼをコードする遺伝子などが挙げられる。

上記(C)において用いる宿主としては、大腸菌をはじめとする原核生物、酵母、真菌等の微生物、及び昆虫や動物等の細胞のいずれでも良いが、用いる発現ベクターに適したものを選択する必要がある。微生物の例としては、エシュリヒア コリ(*Escherichia coli*)の菌株、たとえば*E. coli* K12株294(ATCC 31446)、*E. coli* X1776(ATCC 31537)、*E. coli* C600、*E. coli* JM109、*E. coli* B株、あるいはバチラス サブチリス(*Bacillus subtilis*)の如き*Bacillus*属の菌株、あるいはサルモネラ チフィムリウム(*Salmonella typhimurium*)またはセラチア マーゼサンス(*Serratia marcesans*)等の大腸菌以外の腸内菌、あるいはシュードモナス(*Pseudomonas*)属の種々の菌株が挙げられる。酵母としては、たとえば、サッカロミセス セレビシエ(*Saccharomyces cerevisiae*)、シゾサッカロマイセス ポンベ(*Schizosaccharomyces pombe*)、ピキア パストリス(*Pichia pastoris*)などが用いられる。真菌としては、たとえば、アスペルギルス

ニドランス (*Aspergillus nidulans*)、アクレモニウム ク
リソゲナム (*Acremonium chrysogenum*) (ATCC 11
550) 等が挙げられる。

昆虫細胞としては、たとえば、ウイルスがAcNPVの場合は、夜盗蛾の幼虫
由来株化細胞 (*Spodoptera frugiperda*: Sf細胞)、*Tr*
*ichoplusia ni*の卵由来のHigh Five TM細胞、などが用
いられる。動物細胞の例としては、HEK 293細胞、COS-1細胞、COS
-7細胞、HeLa細胞、チャイニーズハムスター (CHO) 細胞等が挙げられ
る。これらの中でも、CHO細胞およびHEK 293細胞が好ましい。細胞を
宿主とする場合、用いられる発現ベクターと宿主細胞の組合せは実験の目的によ
り異なるが、その組合せにより、一過的発現、構成的発現の2種類の発現方式が
考えられる。

上記 (C) における微生物及び細胞の形質転換とは、DNAを強制的方法や、
細胞の貪食能により微生物や細胞に取り込ませ、プラスミド状態あるいは染色体
に組み込まれた状態でDNAの形質を一過的あるいは構成的に発現させることで
ある。当業者であれば公知の方法によって形質転換できる (たとえば実験医学別
冊遺伝子工学ハンドブック)。たとえば動物細胞の場合、DEAE-デキストラン
法、リン酸カルシウム法、エレクトロポレーション法 (電気穿孔法)、リポフェク
ション法などの方法でDNAを細胞に導入することができる。動物細胞を用いて、
本発明のタンパク質を安定に発現させる方法としては、上記の動物細胞に導入さ
れた発現ベクターが染色体に組み込まれた細胞をクローン選択によって選択する
方法がある。具体的には、上記の選択マーカーを指標にして形質転換体を選択す
る。さらに、このように選択マーカーを用いて得られた動物細胞に対して、繰り
返しクローン選択を行なうことにより本発明のタンパク質の高発現能を有する安
定な動物細胞株を得ることができる。また、*Dihydrofolate re*
ductase (DHFR) 遺伝子を選択マーカーとして用いた場合*Metho*
trexate (MTX) 濃度を徐々に上げて培養し、耐性株を選択することによ
り、DHFR遺伝子とともに、本発明のタンパク質をコードするDNAを細胞
内で増幅させて、さらに高発現の動物細胞株を得ることもできる。

上記の形質転換された細胞を本発明のタンパク質をコードするDNAが発現可能な条件下で培養し、本発明のタンパク質を生成、蓄積せしめることによって、本発明のタンパク質を製造することができる。すなわち、本発明は、上記（３）～（６）に記載の単離されたポリヌクレオチドを含む形質転換された細胞を、該ポリヌクレオチドによりコードされているタンパク質を発現させる条件下培養し、次いで培養物から該タンパク質を回収することを含む該タンパク質の製造方法である。

上記の形質転換された細胞の培養は、当業者に公知の方法で行なうことができる（たとえばバイオマニュアルシリーズ４、羊土社）。たとえば動物細胞の場合、各種の動物細胞培養法、たとえば、シャーレ培養、マルチトレイ式培養、モジュール培養などの付着培養、または細胞培養用担体（マイクロキャリアー）に付着させるか生産細胞自体を浮遊化させ浮遊培養等の公知の方法により培養を行なえば良い。培地は通常良く用いられる動物細胞用の培地、たとえばD-MEMやRPMI 1640等を用いれば良い。

上記培養物から本発明のタンパク質を分離精製するには、自体公知の分離・精製法を適切に組み合わせて行なうことができる。これらの公知の分離、精製法としては、塩析や溶媒沈澱法などの溶解度を利用する方法、イオン交換クロマトグラフィーなどの荷電の差を利用する方法、透析法、限外ろ過法、ゲルろ過法、およびSDS-ポリアクリルアミドゲル電気泳動法などの主として分子量の差を利用する方法、アフィニティークロマトグラフィーなどの特異的親和性を利用する方法、逆相高速液体クロマトグラフィーなどの疎水性の差を利用する方法、等電点電気泳動法などの等電点の差を利用する方法などが用いられる。たとえば、本発明のタンパク質は、硫酸またはエタノール沈殿、酸抽出、アニオンまたはカチオン交換クロマトグラフィー、ホスフォセルロースクロマトグラフィー、疎水性相互作用クロマトグラフィー、アフィニティークロマトグラフィー、ヒドロキシアパタイトクロマトグラフィーおよびレクチンクロマトグラフィーを含む既知の方法により組換え細胞培養物から回収し、精製することができる。最も好ましくは、高性能液体クロマトグラフィーが精製に使用される。ポリペプチドが細胞内合成、単離または精製の間に変性するときには、活性なコンフォーメーションを再生する

ためにタンパク質をリフォールディングするためのよく知られた技術を使用できる。

本発明のタンパク質を他のタンパク質との融合タンパク質として製造することができる。これらも、本発明に含まれる。この融合タンパク質を発現する際に用いられるベクターとしては、該タンパク質をコードするDNAを組み込むことができ、かつ該融合タンパク質を発現することができるベクターであれば、いかなるベクターでも用いることができる。本発明のペプチドに融合できるタンパク質としては、たとえばグルタチオン-S-トランスフェラーゼ (GST)、ヒスチジン残基の6個の連続配列 ($6 \times \text{His}$) 等が挙げられる。本発明のタンパク質を他の蛋白質と融合した蛋白質として発現させた場合には、融合した蛋白質に親和性をもつ物質を用いたアフィニティークロマトグラフィーを用いて精製することができる。例えば、GSTとの融合蛋白質として生産した場合は、グルタチオンをリガンドとするアフィニティークロマトグラフィーにより精製することができる。

本発明は、上記(7)のタンパク質の活性を阻害するタンパク質を含む。たとえば、抗体や上記(7)のタンパク質の活性中心等に結合し、活性の発現を妨げる他のタンパク質が挙げられる。

本発明は、前記の本発明のタンパク質あるいはその部分ペプチドに特異的に結合する抗体ならびにそのような抗体の製造方法に関する。抗体は、本発明のタンパク質を認識し得る抗体であれば、ポリクローナル抗体、モノクローナル抗体、ならびにこれらの抗体のフラグメント、一本鎖抗体、ヒト化抗体の何れであってもよい。抗体フラグメントは、公知の技術によって作製することができる。たとえば、該抗体フラグメントには、限定されるものではないが、 $F(a b')$ 2フラグメント、 $F a b'$ フラグメント、 $F a b$ フラグメント及び $F v$ フラグメントが含まれる。たとえば、モノクローナル抗体またはポリクローナル抗体は、上記(1)または(2)に記載のタンパク質を抗原またはエピトープ含有フラグメントとして非ヒト動物に投与することにより得られる。本発明のタンパク質に対する抗体は、本発明のタンパク質あるいはそのペプチドを抗原として用い、自体公知の抗体または抗血清の製造法に従って製造することができる。たとえば実験医学別冊

新遺伝子工学ハンドブック 改訂第3版に記載の方法が挙げられる。

ポリクローナル抗体の場合であれば、たとえば、本発明のタンパク質をウサギなどの動物に本発明のタンパク質あるいはペプチドを注射することにより該タンパク質あるいはペプチドに対する抗体を産生させ、次いで血液を採取し、これを、たとえば硫酸沈殿、イオン交換クロマトグラフィー、あるいは該タンパク質を固定化したアフィニティーカラム等によって精製することで調製することができる。

モノクローナル抗体の場合は、たとえば、本発明のタンパク質をマウスなどの動物に免疫し、同マウスから脾臓を抽出し、これをすりつぶして細胞にし、マウスミエローマ細胞とポリエチレングリコールなどの試薬により融合させ、これによりできた融合細胞（ハイブリドーマ）の中から、本発明のタンパク質に対する抗体を産生するクローンを選択する。次いで、得られたハイブリドーマをマウス腹腔内に移植し、同マウス内より腹水を回収し、得られたモノクローナル抗体を、たとえば硫酸沈殿、イオン交換クロマトグラフィー、あるいは該タンパク質を固定化したアフィニティーカラム等によって精製することで調製することができる。

得られた抗体をヒトに投与する目的で使用する場合は、免疫原性を低下させるために、ヒト型化抗体あるいはヒト抗体を用いることが好ましい。ヒト型化抗体は、トランスジェニックマウスまたは他の哺乳動物を用いて作製することができる。これらのヒト型化抗体のやヒト抗体の一般的概説は、たとえば、M o r r i s o n, S. L. e t a l. [P r o c. N a t l. A c a d. S c i. U S A, 81:6851-6855 (1984)], J o n e s, P. T. e t a l [N a t u r e 321:522-525 (1986)], 野口浩 [医学のあゆみ 167:457-462 (1993)], 松本隆志 [化学と生物 36:448-456 (1998)] によって供されている。ヒト化キメラ抗体は、マウス抗体のV領域とヒト抗体のC領域を遺伝子組換えにより結合し、作製することができる。ヒト化抗体は、マウスのモノクローナル抗体から相補性決定部位（CDR）以外の領域をヒト抗体由来の配列に置換することによって作製できる。また、免疫系をヒトのものと入れ換えたマウスを用いて、該マウスを免疫して、通常のモノクローナル抗体と同様に直接ヒト抗体を作製することもできる。これらの抗体は、タンパク質を発現するクローンを単離したり同定するのに使用できる。また、こ

これらの抗体は、本発明のタンパク質を細胞抽出液、または本発明のタンパク質を産生する形質転換細胞から精製するのに使用できる。更にこれらの抗体は、細胞や組織中の本発明のタンパク質を検出するE L I S AやR I A（ラジオイムノアッセイ）、またはウエスタンブロット系の構築に使用できる。このような検出系は、動物、好ましくは、ヒトの組織または血管内流体などの身体サンプル中に存在する本発明のタンパク質の存在量を検出する診断目的に使用することができる。たとえば、これらの抗体は、炎症、自己免疫疾患、感染症（一例としてH I V感染）、骨疾患、癌などの、本発明のタンパク質の（発現）異常に起因するN F - κ Bの望ましくない活性化または抑制によって特徴付けられる疾患の診断に使用できる。疾患の診断の基礎を提供するために、本発明のタンパク質の発現についての通常の値、すなわち標準値が確立されなければならないが、これは当業者においては周知の技術である。すなわち、複合体形成のための適切な条件下で、ヒトあるいは動物のどちらでもよいが、正常の被験者から得られた体液あるいは細胞抽出物と、本発明のタンパク質に対する抗体とを結合させ、この抗体-タンパク複合体の量を化学的または物理的手段により検出し、これを既知量の抗原（本発明のタンパク質）を含む標準液を用いて作成した標準曲線を用いて、正常サンプルから得られた標準値を算出する。標準値と本発明のタンパク質が関係する疾患を潜在的に患う被験者からのサンプルから得られた値と比較し、標準値との偏差によって疾病の存在を確認することができる。また、これらの抗体は、本発明のタンパク質の機能を研究する試薬としても用いることができる。

本発明の抗体は精製され得、次いで、たとえば、炎症、自己免疫疾患、感染症（一例としてH I V感染）、癌などの、本発明のタンパク質の（発現）異常に起因するN F - κ Bの望ましくない活性化によって特徴付けられる疾患の患者に投与され得る。すなわち本発明は、上記に記載の抗体を有効成分として含有する医薬、および抗体を用いた治療方法である。これらの医薬は治療的使用のためにさらなる有効成分または不活性成分（たとえば、従来の薬学的に受容可能なキャリアまたは希釈剤（たとえば、免疫原性アジュバント）と、生理学的に無毒の安定化剤および賦形剤とともに組み合わせられ得る。これらの組み合わせは、濾過滅菌され、そして凍結乾燥により投薬バイアル中に、または安定化水性調製物中の貯蔵物と

して投薬形態にされ得る。患者への投与は、たとえば、動脈内注射、静脈内注射、皮下注射などの当業者に公知の方法により行い得る。投与量は、患者の体重や年齢、投与方法などにより変動するが、当業者であれば適当な投与量を適宜選択することが可能である。これらの抗体は、本発明のタンパク質で仲介されるNF- κ Bの活性化を阻害し、治療効果を示す。

本発明のDNAは、細胞内シグナリングプロセスに関与する他のタンパク質を単離、同定、クローン化することにも使用できる。たとえば、本発明のタンパク質をコードするDNA配列は、コードされたタンパク質を「バイト (b a i t)」として用いて、cDNAまたはゲノムDNAライブラリーから、本発明のタンパク質に結合できるタンパク質をコードする他の配列「プレイ (p r e y)」を単離し、クローン化する酵母ツーハイブリッドシステム（たとえばNature、340:245-246 (1989)）に用いることができる。同様の方式で、本発明のタンパク質が、他の細胞タンパク質（たとえばNIK, TRAF2）に結合できるかどうかを決定することができる。あるいは別の方法として、本発明のタンパク質の抗体を用いた免疫沈降法（たとえば、実験医学別冊新遺伝子工学ハンドブック）によって、本発明のタンパク質に結合し得るタンパク質を細胞抽出物から単離する方法が挙げられる。さらに別の方法として、上記に記載のように、本発明のタンパク質を他のタンパク質との融合タンパク質として発現させ、融合タンパク質に対する抗体を用いて免疫沈降法を行ない、本発明のタンパク質に結合し得るタンパク質を単離する方法が挙げられる。

診断アッセイは、前述の方法により、NF- κ Bを活性化する機能を持つ(1)、(2)または(7)のタンパク質遺伝子中の変異を検出することにより疾患の診断や該疾患への感受性を決定するための方法を提供する。さらに、このような疾患は、個体に由来するサンプル中のタンパク質またはmRNAレベルの異常な減少または増加を測定することを含む方法によって診断してもよい。発現の減少または増加は、当該技術でRNAレベルでのポリヌクレオチドの定量によく知られた方法、たとえば、RT-PCRなどの核酸増幅法、およびRNase保護法、ノーザンブロット法その他のハイブリダイゼーション法などの方法で測定できる。宿主に由来するサンプル中のタンパク質レベルの測定に使用され得るアッセイ技

術は、当業者によく知られている。そのような方法には、ラジオイムノアッセイ、競合的結合測定法、ウェスタンブロット分析およびE L I S Aアッセイが含まれる。本発明のDNAは、本発明のタンパク質またはそのペプチドフラグメントをコードするDNAまたはmRNAにおける異常を検出するのに使用できる。本発明は、個体における上記（１）、（２）または（７）に記載のタンパク質の発現に関連した疾患または疾患への感受性を診断する方法に関する。該方法は、タンパク質をコードするポリヌクレオチド配列における変異を、測定することを含む。

本発明のDNAは、本発明のDNAを用いることによって、本発明のタンパク質またはその部分ペプチドをコードするDNAまたはmRNAの異常を検出することができるので、たとえば、該DNAまたはmRNAの損傷、突然変異あるいは発現低下や、増加あるいは発現過多などの遺伝子診断に有用である。すなわち本発明は、個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法であって、

（a）個体のゲノムにおける請求項１、２または７に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、および／または

（b）該個体に由来するサンプル中での該タンパク質の発現量を分析する、ことを含む診断方法であって、好ましくは発現するタンパク質の量が正常の２倍以上あるいは１／２以下の場合に病気であると診断する方法に関する。

上記（a）により、NF- κ Bを活性化する機能を持つ（１）、（２）または（７）のタンパク質をコードするヌクレオチド配列に変異がある場合は、該変異がNF- κ Bの活性化に関連した疾病を引き起こす可能性がある。あるいは、（b）により、被験者における前記（１）、（２）または（７）のタンパク発現量を測定し正常値を異なる値を示す場合は、NF- κ Bを活性化する作用を持つ本発明の新規タンパク質の発現量異常がNF- κ Bの活性化に関連した疾病の原因である可能性がある。ここで、（a）のNF- κ Bを活性化する機能を持つ（１）、（２）または（７）のタンパク質をコードするヌクレオチド配列の変異の有無を測定する方法としては、それらのタンパク質をコードする遺伝子のヌクレオチド配列の一部をプライマーとして、RT-PCRを行い、その後通常のヌクレオチド配列決定方法によって配列を決定し、変異の有無を検出できる。あるいは、PCR-SS

CP法 (Genomics、5:874-879、1989年、実験医学別冊新遺伝子工学ハンドブック) によっても変異の有無を調べることができる。

また、(b) のタンパク質発現量を調べる方法としては、たとえば、前記(16)に記載の抗体を利用する方法が挙げられる。

また、本発明は、本発明のタンパク質によるNF- κ Bの活性化を阻害または促進する化合物のスクリーニング方法に関する。

このスクリーニング方法は、

(a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子および検出可能なシグナルを提供し得る成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で形質転換された宿主細胞を培養する工程、

(c) 該形質転換された細胞と1あるいは複数個の被検化合物とを接触させる工程、

(d) 検出可能なシグナルを検出する工程、および

(e) 該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物を離または同定する工程、を含む。

また、シグナルを正常より2倍以上増加させる化合物を活性化剤化合物として単離または同定し、2分の1以下に減少させる化合物を阻害剤化合物として単離または同定することが好ましい。

検出可能なシグナルを提供し得る成分としては、たとえばレポーター遺伝子が挙げられる。レポーター遺伝子は、テストを行なう転写因子の活性化を直接検出するかわりに用いられるもので、調べたい遺伝子のプロモーターをレポーター遺伝子につなぎ、レポーター遺伝子の産物の活性を測定することによってプロモーターの転写活性の解析を行なうものである(バイオマニュアルシリーズ4、羊土社(1994))。

レポーター遺伝子としては、その発現産物の活性または生産量(mRNAの生産量も含まれる)を当業者が測定可能なものであれば、いかなるペプチド、タンパク質をコードする遺伝子も用いることができる。たとえば、クロラムフェニコ

ールアセチルトランスフェラーゼ、 β -ガラクトシダーゼ、ルシフェラーゼ等の酵素活性を測定することで利用できる。NF- κ Bの活性化を評価するのに用いるレポータープラスミドとしては、NF- κ B認識配列をレポーター遺伝子の上流に組み込んだものであればよく、たとえばpNF- κ B-Luc (STRATAGENE社)が利用できる。あるいは、Tanaka S. et al. J. Vet. Med. Sci. Vol. 59 (7)、Rothe M. et al. Science Vol. 269 p1424-1427 (1995)に記載のNF- κ B依存レポータープラスミドが例示される。

宿主細胞としては、NF- κ Bの活性化を検出し得る細胞であればよく、好ましくは、哺乳動物細胞であり、たとえば293-EBNA細胞が好適に用いられる。形質転換及び培養に関しては、上記に記載の通りである。

NF- κ Bの活性化を阻害または促進する化合物のスクリーニングは、具体的には、たとえば、一定時間培養した形質転換細胞に、被験物質を任意の量添加し、一定時間後の該細胞が発現するレポーター活性を測定し、被験物質を添加しない細胞のレポーター活性と比較することにより、NF- κ Bの活性化を阻害または促進する化合物をスクリーニングすることができる。レポーター活性の測定は、当業者に公知の方法(たとえばバイオマニュアルシリーズ4、羊土社(1994))で行なうことができる。スクリーニングの被検物質には特に制限はなく、低分子化合物、ペプチドなどが挙げられる。被検物質は、人工的に合成したものであっても、天然に存在するものであっても良い。また単一物質でも、混合物でもい。検出可能なシグナルとしては、上記レポーター遺伝子の他に、NF- κ Bの活性化によって発現が誘導されることが知られている、たとえばIL-1やTNF- α のmRNA量あるいはタンパク質量を測定しても良い。mRNA量の測定は、たとえばノーザンハイブリダイゼーションやRT-PCR法などが挙げられる。タンパク質量の測定はたとえば抗体を用いる方法が挙げられる。抗体は公知の方法によって作製しても良いし、市販のもの(たとえば和光純薬工業株式会社)を使用することもできる。

また、以下の(a)～(f)の工程により医薬組成物を製造することも可能である。

(a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子および検出可能なシグナルを与えることができる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で形質転換された宿主細胞を培養する工程、

(c) 該形質転換された宿主細胞と1あるいは複数個の化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、

(e) 該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物を単離または同定する工程、および

(f) 単離または同定された化合物を医薬組成物として最適化する工程。

また、本発明においてシグナルを正常より2倍以上増加させる化合物を活性化剤化合物、2分の1以下に減少させる化合物を阻害剤化合物として単離または同定することが好ましい。

本願発明のタンパク質は、以下の工程により、該タンパク質のアゴニスト、アンタゴニストまたは阻害剤を、構造を基礎にして設計する方法に使用してもよい。

(a) まず、タンパク質の三次元構造を決定する工程、

(b) アゴニスト、アンタゴニストまたは阻害剤の反応性部位または結合部位と思われる部位の三次元構造を推論する工程、

(c) 推論した結合部位または反応性部位に結合するかあるいは結合すると予測される候補化合物を合成する工程、および

(d) 該候補化合物が本当にアゴニスト、アンタゴニストまたは阻害剤であるか否かを試験する工程。

また本発明は、上記スクリーニングによって得られた化合物を含む。しかしながら、本発明のスクリーニング方法は、上記の方法に限定されるものではない。さらに、上記(14)に記載の方法により医薬組成物を製造する方法も含む。

該候補化合物には特に制限はなく、低分子化合物、ペプチドなどが挙げられ、また、人工的に合成したものであっても、天然に存在するものであっても良い。上記スクリーニングによって得られた化合物は、NF- κ Bの活性化を阻害または促進する作用を有しているので、NF- κ Bの望ましくない活性化あるいは不

活性化に起因する疾患を治療または予防するための医薬として有用である。混合物から目的化合物を単離、精製するには、自体公知の方法、例えば濾過、抽出、洗浄、乾燥、濃縮、結晶化、各種クロマトグラフィー等を適宜組み合わせて行うことができる。化合物の塩を取得したい時は、化合物が塩の形で得られる場合にはそのまま精製すれば良く、また遊離の形で得られる場合には、通常の方法により適当な溶媒に溶解または懸濁し、所望の酸または塩基を添加し、塩を形成させて単離精製すれば良い。本発明の方法を用いて得られる化合物またはその塩を医薬組成物として最適化する工程としては、例えば以下のような常法により製剤化する方法が例示される。すなわち活性成分として有効な量の上記化合物またはその薬理的に許容される塩と、薬理的に許容される担体とを混合すれば良い。製剤化は選択された投与様式に適した形態が選ばれる。経口投与に適した組成物としては、錠剤、顆粒剤、カプセル剤、丸剤、および散剤などの固体形態、溶液剤、シロップ剤、エリキシル剤、および懸濁液剤などの液体形態が挙げられる。非経口投与に有用な形態としては、無菌溶液剤、乳剤、および懸濁液剤が挙げられる。上記の担体としては、例えばゼラチン、乳糖、グルコース等の糖類、コーン・小麦・米・とうもろこし澱粉等の澱粉類、ステアリン酸等の脂肪酸、ステアリン酸カルシウム・ステアリン酸マグネシウム等の脂肪酸塩、タルク、植物油、ステアリンアルコール・ベンジルアルコール等のアルコール、ガム、ポリアルキレングリコール等が挙げられる。これらのうち液状担体の例としては、一般に水、生理食塩水、デキストロースまたは類似の糖溶液、エチレングリコール、プロピレングリコール、ポリエチレングリコール等のグリコール類が挙げられる。

本発明は、NF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットである。該キットは、

(a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子およびNF- κ Bの活性化後、その活性化が検出可能なシグナルを提供する成分を含有する細胞、

(b) 該検出可能なシグナルを測定するための試薬、から成り、NF- κ Bの活性化を阻害または促進する化合物をスクリーニングするために必要な試薬類を含む。

別の側面において、本発明は、

(a) 配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179で表されるヌクレオチド配列を有する本発明のポリヌクレオチド；

(b) (a) のヌクレオチド配列に相補的なヌクレオチド配列；

(c) 配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180で表されるアミノ酸配列を有する本発明のタンパク質またはそれらの断片；または

(d) (c) の本発明のタンパク質に対する抗体；
を含む診断キットに関する。

少なくとも (a) ~ (d) のいずれかを含むキットは、炎症、自己免疫疾患、感染性疾患（たとえばH I V感染）および癌などの疾患または該疾患への感受性を診断するのに有用である。

N F - κ B は、炎症、自己免疫疾患、ガン及びウイルス感染などの多種の病理学的状態におけるその関与のため、薬物デザイン及び治療介入のための魅力的な

標的である。多数の実験が、NF- κ B活性が深い生理学的作用を有し得ることを示している(たとえば、Ann. Rheum. Dis. 57, 738-741 (1998), American Journal of Pathology 152, 793-803 (1998), ARTHRITIS & RHEUMATISM 40, 226-236 (1997), Am. J. Respir. Crit. Care Med. 158, 1585-1592 (1998), J. Exp. Med. 188 1739-1750 (1998), Gut 42, 477-484 (1998), The Journal of Immunology 161, 4572-4582 (1998), Nature Medicine 3, 894-899 (1997))。本明細書中に報告するNF- κ Bを活性化する作用を有する新規タンパク質の発見により、異常なNF- κ B機能を制御する新しい方法が提供された。さらなる具体例において、本発明は、NF- κ Bの活性化を阻害するための前記のNF- κ Bを活性化する作用を有するタンパク質の機能を阻害する化合物を用いる方法に関する。また、本発明は、NF- κ Bの活性化を促進するための前記のNF- κ Bを活性化する作用を有するタンパク質の機能を活性化する化合物を用いる方法に関する。上記スクリーニング方法によって得られた、NF- κ Bの活性化を阻害する化合物は、たとえば炎症、自己免疫疾患(慢性関節リウマチ、全身性エリテマトーデス、喘息など)、感染症、骨疾患、移植片拒絶反応などの、NF- κ Bの望ましくない活性化によって特徴つけられる疾患を治療または予防する医薬として有用である。更に、NF- κ Bの活性化が細胞のアポトーシスを抑制することが、最近明らかになりつつある。上記スクリーニング方法によって得られた、NF- κ Bの活性化を阻害する化合物は、アポトーシスを促進する機能を持つ可能性も考えられる。アポトーシスの誘導が治療につながる疾患としては、腫瘍が挙げられる。

また、NF- κ B活性の異常に関連する疾患としては、例えば、AIDS (acquired immunodeficiency syndrome)、神経変性疾患(アルツハイマー病、パーキンソン病、筋萎縮性側索硬化症など)、虚血性障害(心筋梗塞、再灌流障害などにより起こるものなど)、骨髓形成不良症候群(再生不良性貧血など)、皮膚疾患(Toxic epidermal necrolysis など)、増殖性腎炎(IgA腎炎、紫斑病性腎炎、ループス腎炎)、劇症肝炎などが挙げられる。よって、上記スクリーニング方法によって得られた、NF- κ B活性化を阻害する化合物または促進する化合物はこれらの疾患の治療または予防のための医薬として有用である。

更に、本発明のタンパク質をコードする遺伝子は、癌、自己免疫疾患、アレルギー

ギー性疾患、および炎症性応答を初めとする様々な疾患の治療を目的とした遺伝子治療にも有用である。遺伝子治療とは、疾病の治療を目的として、遺伝子または遺伝子を導入した細胞をヒトの体内に投与することを意味する。本発明のタンパク質や該タンパク質をコードする DNA は、診断目的にも使用できる。

本発明のスクリーニング方法を用いて得られる化合物またはその塩を上述の医薬組成物として使用する場合、常套手段に従って実施することができる。たとえば、錠剤、カプセル剤、エリキシル剤、マイクロカプセル剤、無菌性溶液、懸濁液剤などとすることができる。このようにして得られる製剤は安全で低毒性であるので、たとえば、ヒトや哺乳動物（たとえば、ラット、ウサギ、ヒツジ、ブタ、ウシ、ネコ、イヌ、サルなど）に対して投与することができる。患者への投与は、たとえば、動脈内注射、静脈内注射、皮下注射など当業者に公知の方法により行う。投与量は、患者の体重や年齢、投与方法などにより変動するが、当業者であれば適当な投与量を適宜選択することが可能である。また、該化合物が DNA によりコードされうるものであれば、該 DNA を遺伝子治療用ベクターに組み込み、遺伝子治療を行うことも考えられる。投与量、投与方法は、患者の体重や年齢、症状などにより変動するが、当業者であれば適宜選択することが可能である。すなわち本発明は、上記化合物を有効成分として含有する医薬に関する。

さらに、上記化合物は、炎症、自己免疫疾患、ウイルス性疾患、感染症、ガン、骨疾患などの、NF- κ B 活性の異常によって特徴つけられる疾患を治療または予防する医薬として有用である。すなわち本発明は、上記化合物を含む炎症、自己免疫疾患、ウイルス性疾患、感染症、ガン、骨疾患などの医薬に関する。具体的には、例えば、慢性関節リウマチ、変形性関節症、全身性エリテマトーデス、糖尿病、敗血症、喘息、アレルギー性鼻炎、虚血性心疾患、炎症性腸疾患、くも膜下出血、ウイルス肝炎、エイズ、アテローム性動脈硬化症、アトピー性皮膚炎、ウイルス感染症、クローン病、糖尿病、通風、肝炎、多発性硬化症、心筋梗塞、腎炎、骨粗鬆症、アルツハイマー、パーキンソン病、ハンチントン舞踏病、乾癬、筋萎縮性側索硬化症、心筋梗塞、再生不良性貧血などに対する治療及び予防薬として有用である。

さらにまた、本発明は、炎症、自己免疫疾患、ウイルス性疾患、ガン、感染症、

骨疾患などの医薬の製造における上記（１４）記載の方法により製造された医薬組成物の使用も含む。また本発明は、上記（３）～（６）に記載の遺伝子に対するアンチセンスオリゴヌクレオチドである。アンチセンスオリゴヌクレオチドは、標的とした遺伝子配列に対して相補的な配列を持つオリゴヌクレオチドを用いて、タンパク質への翻訳、細胞質への輸送、あるいは全体的な生物活性機能に必要な他の活性等のRNAの機能を阻害することによって、標的遺伝子の発現を抑制することができる。この際、アンチセンスオリゴヌクレオチドとしては、RNAを用いても良いし、DNAを用いても良い。本発明のDNA配列は、本発明のタンパク質をコードする遺伝子から転写されたmRNAとハイブリダイズし得るアンチセンスオリゴヌクレオチドを作製するために使用できる。一般にアンチセンスオリゴヌクレオチドが、その遺伝子の発現に対して抑制的に作用することは公知での事実である（たとえば、細胞工学 Vol. 13 No. 4 (1994)）。本発明のタンパク質をコードする遺伝子に対するアンチセンスコード配列を有するオリゴヌクレオチドは、標準の方法で細胞内に導入することができ、該オリゴヌクレオチドは、本発明のタンパク質をコードする遺伝子のmRNAの翻訳を効果的に遮断して、その発現を遮断して、望ましくない作用が阻害される。

本発明のオリゴヌクレオチドは、天然に見出されるオリゴヌクレオチドの他に、修飾されたものであっても良い〔たとえば、村上&牧野：細胞工学 Vol. 13 No. 4 p 259-266 (1994)、村上章：蛋白質核酸酵素 Vol. 40 No. 10 p 1364-1370 (1995)、竹内恒成ら：実験医学 Vol. 14 No. 4 p 85-95 (1996)〕。従って、オリゴヌクレオチドは変化した糖部分あるいは糖間部分を有していても良い。これらの例は、当該技術分野において使用が知られているホスホチオエート及び他のイオウ含有種である。幾つかの好ましい態様に従えば、オリゴヌクレオチドの少なくとも一つのホスホジエステル結合が、その活性が調節されるべきRNAが位置する細胞の領域に浸透する組成物の能力を高める機能を有する構造により置換される。

このような置換は、ホスホチオエート結合、ホスホアミデート結合、メチルホスホネート結合または短鎖アルキルもしくはシクロアルキル構造を含むことが好ましい。オリゴヌクレオチドはまた、少なくとも幾つかの修飾されたヌクレ

オチド型を含んでいても良い。従って、天然に通常見いだされるもの以外のプリン及びピリミジンを使用していても良い。同様に本発明の本質的な意図が実行される限り、ヌクレオチドサブユニットのフラノシル部分を修飾することもできる。このような修飾の例は、2'-O-アルキル-、及び2'-ハロゲン置換ヌクレオチドである。本発明において有用な幾つかの糖部分の2'位の修飾の例は、OH、SH、SCH₃、OCH₃、OCN、またはO(CH₂)_nCH₃（ここでnは1から約10である）、及び同様の特性を有する他の置換基である。全てのこのような類似体は、本発明の遺伝子のmRNAとハイブリダイズしてそのRNAの機能を阻害する機能を果たす限り、本発明に包含される。

本発明のオリゴヌクレオチドは、約3から約50ヌクレオチドを含み、約8から約30ヌクレオチドを含むことが好ましく、約12から約25ヌクレオチドを含むことがさらに好ましい。本発明のオリゴヌクレオチドは、周知の方法である固相合成法により作製することができる。このような合成のための装置は、Applied Biosystemsを含む幾つかの業者により販売されている。ホスホチオエート等の他のオリゴヌクレオチドの製造も当業者に公知の方法で作製できる。

本発明のオリゴヌクレオチドは、本発明の遺伝子から転写されるmRNAとハイブリダイズできるように設計される。与えられた遺伝子の配列に基づいてアンチセンスオリゴヌクレオチドを設計する方法は、当業者であれば容易である〔たとえば、村上および牧野：細胞工学 Vol. 13 No. 4 p259-266 (1994)、村上章：蛋白質核酸酵素 Vol. 40 No. 10 p1364-1370 (1995)、竹内恒成ら：実験医学 Vol. 14 No. 4 p85-95 (1996)〕。最近の研究は、mRNAの5'領域、好ましくは翻訳開始部位を含む領域に設計されたアンチセンスオリゴヌクレオチドが、遺伝子の発現の阻害に最も効果的であることを示唆している。アンチセンスオリゴヌクレオチドの長さは、15から30ヌクレオチドが好ましく、20から25ヌクレオチドがより好ましい。ホモロジー検索で他のmRNAとの相互作用がないこと、オリゴヌクレオチド配列内で二次構造を取らないことを確認しておくことは重要である。設計したアンチセンス分子が機能したかどうかの評価は、適当な細胞を

用いて、該細胞にアンチセンスオリゴヌクレオチドを導入し、当業者には公知の方法で、対象mRNAの量（たとえば、ノーザンブロットまたはRT-PCR法）、あるいは対象タンパク質の量（たとえば、ウエスタンブロットまたは蛍光抗体法）を測定することにより、発現抑制の効果を確認できる。

一方、三重らせん形成（トリプル・ヘリックス技術）は、核内のDNAを標的とした、主に転写の段階での遺伝子発現制御方法である。オリゴヌクレオチドは、主に転写に関与する遺伝子領域に設計され、それにより、転写及び本発明のタンパク質の産生を抑える。これらのRNA、DNA、オリゴヌクレオチドは、公知の合成装置などを用いて製造することができる。

本発明のオリゴヌクレオチドは、標的核酸配列を含む細胞に、たとえばリン酸カルシウム法、リポフェクション法、エレクトロポレーション法、マイクロインジェクション法などのDNAトランスフェクション法、またはウイルスなどの遺伝子導入ベクターの使用を含む遺伝子導入法のいずれを用いて導入してもよい。適切なレトロウイルスベクターを用いてアンチセンスオリゴヌクレオチド発現ベクターを作製し、その後、該発現ベクターを細胞と*in vivo*または*ex vivo*で接触させることにより、標的核酸配列を含む細胞に導入できる。

本発明のDNAは、アンチセンスRNA/DNA技術またはトリプル・ヘリックス技術を用いて、本発明のタンパクを介するNF- κ Bの活性化を阻害するのに使用できる。

本発明のタンパク質をコードする遺伝子のアンチセンスオリゴヌクレオチドは、たとえば炎症、自己免疫疾患、感染症（たとえば、HIV感染症）、ガンなどの、NF- κ Bの望ましくない活性化によって特徴つけられる疾患を治療または予防する医薬として有用である。すなわち、本発明は、上記アンチセンスオリゴヌクレオチドを有効成分として含有する医薬である。また、本発明のアンチセンスオリゴヌクレオチドは、ノーザンハイブリダイゼーション法またはPCR法を用いてそれらの疾病の検出に利用することもできる。

本発明は、NF- κ Bの活性化を阻害するリボザイムも含む。リボザイムは、核酸のヌクレオチド配列を認識して、核酸を切断する活性を持つRNAである（たとえば、柳川弘志 実験医学バイオサイエンス12、RNAのニューエイジ）。リ

ボザイムは、選択された標的RNA、たとえば本発明のタンパク質をコードするmRNAを開裂するように製造することができる。本発明のタンパク質をコードするDNAのヌクレオチド配列を基に、本発明のタンパク質のmRNAを特異的に切断するリボザイムを設計することができ、かようなリボザイムは本発明のタンパク質のmRNAに対して相補的な配列を有し、該mRNAと相補的結合し、ついで該mRNAが開裂され本発明のタンパク質の発現が減少する（または完全に発現しない）。発現減少のレベルは標的細胞内でのリボザイム発現のレベルに依存している。

よく用いられるリボザイムには、ハンマーヘッド型とヘアピン型の2種類があり、特にハンマーヘッド型リボザイムは切断活性に必要な一次構造や二次構造がよく調べられており、当業者であれば、本発明のタンパク質をコードするDNAのヌクレオチド配列情報のみで容易にリボザイムの設計が可能である〔たとえば、飯田ら：細胞工学 Vol. 16 No. 3, p438-445 (1997)、大川&平比良：実験医学 Vol. 12 No. 12 p83-88 (1994)〕。ハンマーヘッドリボザイムは、標的RNAと相補鎖を形成する2ヶ所の認識部位（認識部位Iと認識部位II）と活性部位からなる構造をなし、標的RNAと認識部位で相補対を形成した後、標的RNAのNUXの配列（N：AまたはGまたはCまたはU、X：AまたはCまたはU）の3'末端側で切断することが知られており、特にGUC（あるいはGUA）が一番高い活性を持つことが知られている〔たとえば Koizumi, M ら :Nucl. Acids Res. 17, 7059-7071 (1989)、飯田ら：細胞工学 Vol. 16 No. 3, p438-445 (1997)、大川&平比良：実験医学 Vol. 12 No. 12 p83-88 (1994)、川崎&多比良：実験医学 Vol. 18 No. 3 p381-386 (2000)〕。

そこでまず、本発明のDNA配列の中からGTC（またはGTA）の配列を探し出し、その前後で数ヌクレオチドから十数ヌクレオチドの相補対をつくるようにリボザイムを設計する。設計したリボザイムの適切性の評価は、たとえば、大川&平比良の文献〔実験医学 Vol. 12 No. 12 p83-88 (1994)〕に記載の方法によって、作製したリボザイムが、インビトロで標的mRNAを切断できるかどうかを調べることで評価できる。リボザイムの調製は、RNA分子を合成するための当分野で周知の方法により調製する。

別法としては、リボザイムの配列をDNA合成機で合成し、たとえばT7或いはSP6のような適切なRNAポリメラーゼプロモーターを有する多種のベクターに組み込み、インピットロで酵素的にRNAを合成させる方法が挙げられる。これらのリボザイムは、たとえばマイクロインジェクション法などの遺伝子導入方法によって細胞内に導入できる。あるいは別の方法として、リボザイムDNAを適当な発現ベクターに組み込んで、株細胞、細胞或いは組織内に導入する。選択された細胞中にリボザイムを導入するのに、適切なベクターを使用することができ、たとえばプラスミドベクター、動物ウイルス（たとえばレトロウイルス、アデノウイルス、ヘルペスあるいはワクシニアウイルス）ベクターがこれらの目的に通常用いられる。これらのリボザイムは、本発明のタンパク質で仲介されるNF- κ Bの活性化を阻害する作用を有する。

本発明はまた、機能を有する新規遺伝子の取得方法であり、オリゴキャッピング法を用いて完全長cDNAライブラリーを作製する方法および該機能を有するタンパク質の存在を示すシグナル因子を用いる方法からなる取得方法に関する。シグナル因子には、たとえばレポーター遺伝子が挙げられる。

機能を有する遺伝子（cDNA）を多数取得するためには、不完全長のものが多いcDNAライブラリーを用いると効率が悪い。したがって、全体のクローンの中で、完全長のものの割合が高いライブラリーが必要となる。完全長cDNAは遺伝子から出来るmRNAの完全なコピーのことである。オリゴキャッピング法で作製したcDNAライブラリーは、完全長cDNAの割合が50～80%であり、従来の方法で作製されたcDNAライブラリーと比べて、5～10倍の完全長cDNAクローンの濃縮になっている(菅野純夫:月刊 BIO INDUSTRY Vol. 16 No. 11 p19-26)。完全長cDNAは、遺伝子の機能解析においては、タンパク質発現のために必須なクローンであり、完全長cDNAのクローンそのものが活性測定のための材料として極めて重要なものであるため、遺伝子の機能解析を試みるに際して、完全長cDNAのクローニングは必須の要件である。さらにその配列を決定することで、それがコードするタンパク質の一次配列を確定するための重要な情報となると同時に、遺伝子の全エクソンの配列も分かる。すなわち、完全長cDNAは、遺伝子を同定する上で貴重な情報、たとえばタンパク質の一次配

列、エクソン-イントロン構造、mRNAの転写開始点、プロモーターの位置などを決めるための情報をも与える。

オリゴキャッピング法による完全長cDNAライブラリー作製は、たとえば実験医学別冊新遺伝子工学ハンドブック改訂第3版（1999年）に記載の方法に従い行うことができる。機能を有するタンパク質の存在を示すレポーター遺伝子は、転写因子等のタンパク質因子が結合できる適切な発現制御配列部分（1つまたは複数）と、その転写因子等による活性化を測定できる構造遺伝子部分からなる。構造遺伝子部分は、その発現産物の活性または生産量（mRNAの生産量も含まれる）を当業者が測定可能なものであれば、いかなるペプチド、タンパク質をコードする遺伝子も用いることができる。たとえば、クロラムフェニコールアセチルトランスフェラーゼ、 β -ガラクトシダーゼ、ルシフェラーゼ等を用いることができ、その酵素活性を測定することで利用できる。

本発明において、オリゴキャッピング法とは、鈴木・菅野 実験医学別冊 遺伝子工学ハンドブック改訂第3版に記載のように、BAP, TAP, RNAリガーゼにより、キャップ構造を合成オリゴに置換する方法である。

本発明の方法は、インビトロ（*in vitro*）の系、あるいは細胞を用いて（*cell-based*）の系のどちらの方法でも良く、好ましくは細胞を用いた系である。細胞は、原核大腸菌をはじめとする原核生物、酵母、真菌等の微生物、及び昆虫や動物等の細胞のいずれでも良く、好ましくは動物細胞であり、293-EBNA細胞、NIH3T3細胞が例示できる。

機能を有するタンパク質の存在を示すレポーター遺伝子としては、本願明細書に示したNF- κ B依存レポーター遺伝子の他に、たとえばCREB（cAMP responsive element binding protein）結合配列あるいはAP-1（activator protein-1）結合配列をレポーター遺伝子の発現制御配列部分に有するレポーター遺伝子が挙げられる。たとえば、CREBを活性化する機能を有する遺伝子を取得したい場合は、CREB依存レポータープラスミドとオリゴキャッピング法で作製した完全長cDNAを含む発現ベクターを細胞に共導入し、その中からレポーター活性が上昇した発現ベクターを選ぶことによって、該目的を達成することができる。また、CREBを抑制する機能を有する遺伝子を取得したい場合は、

C R E B 依存レポータープラスミドとオリゴキャッピング法で作製した完全長 c D N A を含む発現ベクターを細胞に共導入し、その中からレポーター活性が減少した発現ベクターを選ぶことによって、該目的を達成することができる。この場合、細胞に何らかの刺激を加えた状態で行なっても良い。c D N A クローン（発現ベクター）の細胞への導入は、1 クローンでも良いし、複数のクローンを同時に導入しても良い。本発明の該方法の一例は、本願明細書実施例に詳細に記述してある。あるいは、完全長 c D N A を含む発現ベクターとレポーター遺伝子を細胞に導入した後、細胞を I L - 1 あるいは T N F - α など刺激し、レポーター活性の上昇の弱いクローンを選ぶことによって、N F - κ B の活性化を抑制する機能を有する遺伝子を取得するためのスクリーニング系を構築することもできる。

しかしながら、本発明の該方法は、この方法に限定されるものではない。また、本発明の c D N A は、完全長 c D N A であるため、その 5' 末端の配列が m R N A の転写開始点であり、該 c D N A 配列をゲノムのヌクレオチド配列と比較することにより、該遺伝子のプロモーター領域を同定することに利用できる。ゲノムのヌクレオチド配列は、データベースに公知の配列として登録されている場合はその配列を利用できる。あるいは、該 c D N A を用いてたとえばハイブリダイゼーションによってゲノムライブラリーからクローニングし、ヌクレオチド配列を決めることもできる。このようにして、本発明の c D N A のヌクレオチド配列をゲノムの配列と比較することによって、その上流に存在する該遺伝子のプロモーター領域を同定することが可能である。さらに、このようにして同定した該遺伝子のプロモーター断片を用いて該遺伝子の発現を調べるレポータープラスミドを作製することができる。レポータープラスミドは、大方の場合、転写開始点からその上流 2 k b、好ましくは転写開始点からその上流 1 k b の D N A 断片をレポーター遺伝子の上流に組み込むことによって作製できる。さらに該レポータープラスミドは、該遺伝子の発現を増強あるいは減弱させる化合物のスクリーニングに利用できる。具体的には例えば、該レポータープラスミドで適当な細胞を形質転換し、一定時間培養した形質転換細胞に、被験物質を任意の量添加し、一定時間後の該細胞が発現するレポーター活性を測定し、被験物質を添加しない細胞のレポーター活性と比較することによりスクリーニングすることができる。これら

も本発明に含まれる。

また本発明は、配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179で表されるヌクレオチド配列のうち少なくとも1以上を含むデータセットおよび／または配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178および180で表されるアミノ酸配列のうち少なくとも1以上を含むデータセットを保存したコンピュータ読み込み可能媒体に関する。

さらに本発明は、上記に記載の媒体上のデータと他のヌクレオチド配列のデータを比較して相同性の算出を行う方法に関する。すなわち、本発明の遺伝子およびアミノ酸配列は、その2次元および3次元構造を決定し、たとえば同様の機能を有する相同性の高いさらなる配列を同定するための貴重な情報源となる。これらの配列をコンピュータ読み込み可能媒体に保存し、ついで既知の高分子構造プログラムにおいて保存したデータを用いて、GCGのような既知検索ツールを用いてデータベースを検索すれば、データベース中の、ある相同性を有する配列を

見出すことは容易である。

コンピュータ読み取り可能媒体は情報またはデータを保存するのに用いる物体のいずれの組成物であってもよく、たとえば、市販フロッピーディスク、テープ、チップ、ハードドライブ、コンパクトディスク、およびビデオディスク等がある。また、本媒体上のデータは、他のヌクレオチド配列のデータと比較して相同性の算出を行なう方法を可能にする。この方法には、本発明ポリヌクレオチド配列を含む第一のポリヌクレオチド配列をコンピュータ読み込み可能媒体中に提供し、次いで、該第一のポリヌクレオチド配列を少なくとも一つの第二のポリヌクレオチドまたはポリペプチド配列と比較して相同性を同定する工程を含む。

本発明はまた、配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179から選択されるヌクレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質に関する。DNAプローブである複数の各種ポリヌクレオチドがスライドガラス等の特別に加工された基質上に固定され、次いで標識された標的ポリヌクレオチドを、固定化されたポリヌクレオチドとハイブリダイズさせ、それぞれのプローブからのシグナルを検出する。得られるデータは、解析され、遺伝子発現が測定される。

本発明はさらにまた、配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、1

11、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質に関する。このタンパク質を固定した不溶性基質と、生物由来の細胞抽出液とを混合し、不溶性基質上に捕獲された、診断あるいは新薬開発のために有効であることが期待されるタンパク質などの細胞由来の成分を、単離あるいは同定することができる。

実施例

以下に、実施例を挙げて本発明を詳しく説明するが、本発明は、これらの例に何ら限定されるものではない。

(実施例1) オリゴキャッピング法を用いた完全長cDNAライブラリーの作製

(1) ヒト肺線維芽細胞 (Cryo NHLF) からのRNA調製

ヒト肺線維芽細胞 (Cryo NHLF : 三光純薬株式会社より購入) を、添付のプロトコールに従って培養した。10cmシャーレ50枚まで継代培養した後、セルスクレーパーで細胞を回収した。次いで、回収した細胞からRNA抽出用試薬ISOGEN (ニッポンジーンより購入) を用いて全RNAを取得した。取得の具体的方法は、試薬のプロトコールに従った。次いで、オリゴ-dT セルロース カラムを用いて、全RNAからポリA+RNAを取得した。ポリA+RNA取得の具体的方法は、上記Maniatisの実験書に従った。

(2) マウスATDC5細胞からのRNA調製

マウスEC (embryonal carcinoma) 由来クローン化細胞株ATDC5 (Atsumi, T. et al. : Cell Diff. Dev., 30:p109-116 (1990)) を10cmシャーレ50枚まで継代培養した後、上記(1)と同様の方法でポリA+RNAを取得した。ATDC5細胞の培養は、Atsumi, T. et al. : Cell Diff. Dev., 30:p109-116 (1990) に記載の方法に従って培養した。

(3) オリゴキャッピング法による完全長cDNAライブラリー作製

上記ヒト肺線維芽細胞とATDC5細胞のポリA+RNAから、オリゴキャッピング法により完全長cDNAライブラリーをそれぞれ作製した。オリゴキャッピング法による完全長cDNAライブラリー作製の具体的方法は、菅野らの方法〔たとえば、Maruyama, K. & Sugano, S. Gene, 138: 171-174 (1994)、Suzuki, Y. et al. Gene, 200: 149-156 (1997)、鈴木・菅野 実験医学別冊 遺伝子工学ハンドブック改訂第3版〕に従って作製した。

(4) プラスミドDNAの調製

上記実施例で作製した完全長cDNAライブラリーを、エレクトロポレーション法によって大腸菌TOP10株に形質転換した後、100 μ g/mlアンピシリンを含有するLB寒天培地に塗布し、37℃で一晩インキュベートした。続いて、アンピシリン含有LB寒天培地上で生育した大腸菌のコロニーから、QIAGEN社のQIAwell 96 Ultra Plasmid Kitを用いてプラスミドを回収した。具体的方法は、QIAwell 96 Ultra Plasmid Kitに添付のプロトコールに従った。

(実施例2) NF- κ Bを活性化する作用を有するDNAのクローニング

(1) NF- κ Bを活性化する作用を有するタンパク質をコードするcDNAのスクリーニング

293-EBNA細胞(Invitrogen社より購入)を細胞培養用96穴プレートに 1×10^4 Cells/100 μ l/wellとなるように、5% FBS存在下のDMEM培地にまき、24時間37℃で培養した(5% CO₂存在下)。次いで、FuGENE6(Roche社より購入)を用いて、pNF κ B-Luc(STRATAGENE社より購入)50 ngと、上記実施例1.(4)で調製した完全長cDNA発現ベクター2 μ lを1ウエルに共導入した。導入の方法は添付のプロトコールに従った。24時間37℃で培養後、ロングタームルシフェラーゼアッセイシステム、ピッカジーンLT2.0(東洋インキ社)を用いて添付されている説明書に従い、NF- κ Bのレポーター活性(ルシフェラーゼ活性)を測定した。なおルシフェラーゼ活性は、Perkin Elmer社

のWallac ARVOTMST 1420 MULTILABEL COUNTERを用いて行った。

(2) ヌクレオチド配列の決定

上記スクリーニングを155000クローン行い、ルシフェラーゼ活性が対照実験（完全長cDNA発現ベクターの代わりに、空ベクターpME18S-FL3を導入した細胞のルシフェラーゼ活性）と比べて5倍以上上昇しているプラスミドを選抜し、まず、クローニングされているcDNAの5'側（シークエンスプライマー：5'-CTTCTGCTCTAAAAGCTGCG-3'（配列番号181）と3'側（シークエンスプライマー：5'-CGACCTGCAGCTCGAGCACA-3'（配列番号182）からそれぞれone-passシークエンスを行ない、できる限り長く決定した。なお、ヌクレオチド配列決定のための試薬や方法は、Thermo Sequenase II Dye Terminator Cycle Sequencing Kit（アマシャム ファルマシア社）、あるいはBigDye Terminator Cycle Sequencing FS Ready Reaction Kit（アプライド バイオシステムズ社）を用い、ABI PRISM 377シークエンサー、あるいは、ABI PRISM 3100シークエンサーを用い、各々キットに添付されている説明書に従って行なった。

(3) 得られたクローンのデータベース解析

得られたヌクレオチド配列について、GenBankに対するBLAST (Basic local alignment search tool) [S. F. Altschul et al., J. Mol. Biol., 215: 403-410 (1990)] 検索を行なった。その結果、148クローンがNF- κ Bを活性化する作用を有する新規のタンパク質をコードする90種類の遺伝子であった。

(4) 全長シークエンス

90種類の新規のクローンについて全長ヌクレオチド配列（配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、

80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179)を決定し、タンパク質をコードする部分(オープンリーディングフレーム)のアミノ酸配列(配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178および180)を予想した。

(実施例3) NF- κ Bの活性化を阻害する化合物のスクリーニング

293-EBNA細胞を細胞培養用96wellプレートに、 1×10^4 Cells/ 100μ l/wellの細胞数になるように、5%FBS存在下のDMEM培地にまき、5%CO₂存在下、37℃で24時間培養した。次いで、FuGENE6を用いて、上記実施例2で得た、配列番号5、9、17、21、35、37、41、53、57、63、67、71、75、81、87、91、93、97、121、123、129、154、158、162、168、170、172、176または178のNF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子を含む発現ベクター50ngと、レポータープラスミドpNF κ B-Luc50ngを1wellに共導入した。1時間後、プロテアソーム阻害剤であることが知られているMG-132(CALBIOCHEMより購入)(Uehara T. et al. J. Biol. Chem. 274 p15875-15882(1999)、Wang XC. et al. Invest.

O p h t h a l m o l . V i s . S c i . 4 0 p 4 7 7 - 4 8 6) を終濃度 0.1 μ M、0.5 μ M、1.0 μ M、10 μ M になるようにそれぞれ培養液中加入した。37℃で24時間培養後、ピッカジーンLT2.0を用いてレポーター活性を測定した。その結果、MG132はレポーター遺伝子の発現を抑制した(図1から図29)。

産業上の利用性

本発明により、産業上有用性の高いNF- κ Bを活性化する作用を有するタンパク質やそれらの遺伝子が提供された。本発明のタンパク質やそれらの遺伝子により、NF- κ Bの過剰な活性化、又は阻害が関与する疾患の治療や予防に有用な化合物のスクリーニング、さらにそのような疾患の診断薬を作製することが可能である。更に本発明の遺伝子は、遺伝子治療に用いられる遺伝子ソースとしても有用である。

本明細書で引用した全ての刊行物、特許及び特許出願をそのまま参考として本明細書にとり入れるものとする。

請 求 の 範 囲

1. 以下の（a）または（b）の精製されたタンパク質。

（a）配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質。

（b）配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかにおいて1若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつNF- κ B（Nuclear factor kappa B）を活性化する作用を有するタンパク質。

2. 請求項1記載のタンパク質とその全長にわたり95%以上のアミノ酸配列の同一性を有するタンパク質であり、かつNF- κ Bを活性化する作用を有する精製されたタンパク質。

3. 以下の（a）または（b）のタンパク質をコードするヌクレオチド配列を包含する単離されたポリヌクレオチド。

（a）配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178 または 180 のいずれかで表されるアミノ酸配列からなるタンパク質。

（b）配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178 または 180 のいずれかにおいて 1 若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつ NF- κ B を活性化する作用を有するタンパク質。

4. 以下の（a）～（c）のいずれかのポリヌクレオチド配列を含む単離されたポリヌクレオチド。

（a）配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、

48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかで表されるポリヌクレオチド配列。

(b) (a)のポリヌクレオチド配列と相補的なポリヌクレオチド配列を有するポリヌクレオチドとストリンジェントな条件下でハイブリダイズし、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

(c) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかにおいて、1若しくは複数個のヌクレオチドが欠失、置換若しくは付加されたポリヌクレオチド配列からなり、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

5. 請求項3記載のポリヌクレオチドと全長にわたり少なくとも95%以上の同一性を有し、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

6. 請求項4記載のポリヌクレオチドと全長にわたり少なくとも95%以上の

同一性を有し、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

7. 請求項3～6のいずれか1項に記載のポリヌクレオチドによりコードされる精製されたタンパク質。

8. 請求項3～6のいずれか1項に記載のポリヌクレオチドを含有する組換えベクター。

9. 請求項8に記載の組換えベクターを含む形質転換された細胞。

10. 請求項1または2に記載のタンパク質が膜タンパク質である場合における、請求項9記載の細胞の膜。

11. (a) 請求項3～6のいずれか1項に記載の単離されたポリヌクレオチドがコードするタンパク質を発現する条件下で該ポリヌクレオチドを含有する形質転換された細胞を培養し、

(b) 培養物からタンパク質を回収する、
ことを含むタンパク質の製造方法。

12. (a) 個体のゲノムにおける請求項1、2または7に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、および／または

(b) 該個体に由来するサンプル中での該タンパク質の発現量を分析する、
ことを含む、該個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法。

13. 以下の工程を含むNF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングする方法。

(a) NF- κ Bを活性化するタンパク質をコードする遺伝子、およびNF- κ Bの活性化に対応した、検出可能なシグナルを提供しうる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された細胞を培養する工程、

(c) 該形質転換された細胞と1あるいは複数個の候補化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、および

(e) 該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物を単離もしくは同定する工程。

14. 以下の工程を含む、医薬組成物を製造する方法。

(a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子、および検出可能なシグナルを提供しうる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された宿主細胞を培養する工程、

(c) 該形質転換された宿主細胞と1あるいは複数個の候補化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、

(e) 該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物を単離もしくは同定する工程、および

(f) 単離または同定された化合物を医薬組成物として最適化する工程。

15. NF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットであって、

(a) NF- κ Bを活性化するタンパク質をコードする遺伝子、およびNF- κ Bの活性化後、検出可能なシグナルを提供しうる成分により形質転換された細胞、および

(b) 検出可能なシグナルを測定するための試薬

を含むキット。

16. 請求項1、2または7に記載のタンパク質に特異的に結合するモノクローナルあるいはポリクローナル抗体。

17. 請求項1、2または7に記載のタンパク質を抗原あるいはエピトープ含有フラグメントとして非ヒト動物に投与することからなる、請求項1、2または7に記載のタンパク質に特異的に結合するモノクローナルまたはポリクローナル抗体の製造方法。

18. NF- κ Bの活性化タンパク質の発現を阻害する、請求項3～6のいずれか1項に記載のポリヌクレオチドに相補的なアンチセンスオリゴヌクレオチド。

19. 請求項1、2または7に記載のタンパク質をコードするRNAの開裂により、NF- κ Bの活性化を阻害するリボザイム。

20. 炎症、自己免疫疾患、感染症、癌および骨疾患からなる群から選択される疾患の治療に有効な量の請求項13記載の方法でスクリーニングされた化合物および／または請求項16記載のモノクローナルまたはポリクローナル抗体および／または請求項18記載のアンチセンスオリゴヌクレオチドおよび／または請求項19記載のリボザイムを個体に投与することを含む疾患の治療法。

21. NF- κ Bの活性化を阻害または活性化するものとして請求項14に記載の方法により製造された医薬組成物。

22. 炎症、自己免疫疾患、癌、感染症、骨疾患、AIDS、神経変性疾患、または虚血性障害の治療のための請求項21記載の医薬組成物。

23. NF- κ Bに関連する疾患を患っている患者に請求項14記載の方法に

より製造された医薬組成物を投与することからなる炎症、自己免疫疾患、癌、感染症、骨疾患、A I D S、神経変性疾患、または虚血性障害を治療する方法。

2 4. 請求項 1 6 記載のモノクローナルまたはポリクローナル抗体を有効成分として含有する医薬組成物。

2 5. 請求項 1 8 記載のアンチセンスオリゴヌクレオチドを有効成分として含有する医薬組成物。

2 6. 対象疾患が炎症、自己免疫疾患、感染症、癌疾患、骨疾患、A I D S、神経変性疾患および虚血性障害からなる群から選択される、請求項 2 4 または 2 5 に記載の医薬組成物。

2 7. 機能を有する新規遺伝子の取得方法であり、少なくとも以下の工程を含む方法。

(a) オリゴキャッピング法を用いて完全長 c D N A ライブラリーを作製し、
(b) 完全長 c D N A および該機能を有するタンパク質の存在を示すシグナルを発する因子を含有するプラスミドを細胞中にコトランスフェクションし、さらに
(c) シグナルを発するプラスミドを選択する、
方法。

2 8. 配列番号 2、4、6、8、1 0、1 2、1 4、1 6、1 8、2 0、2 2、
2 4、2 6、2 8、3 0、3 2、3 4、3 6、3 8、4 0、4 2、4 4、4 6、
4 8、5 0、5 2、5 4、5 6、5 8、6 0、6 2、6 4、6 6、6 8、7 0、
7 2、7 4、7 6、7 8、8 0、8 2、8 4、8 6、8 8、9 0、9 2、9 4、
9 6、9 8、1 0 0、1 0 2、1 0 4、1 0 6、1 0 8、1 1 0、1 1 2、1 1
4、1 1 6、1 1 8、1 2 0、1 2 2、1 2 4、1 2 6、1 2 8、1 3 0、1 3
2、1 3 4、1 3 6、1 3 8、1 4 0、1 4 2、1 4 4、1 4 6、1 4 8、1 5
0、1 5 1、1 5 3、1 5 5、1 5 7、1 5 9、1 6 1、1 6 3、1 6 5、1 6

7、169、171、173、175、177または179で表されるヌクレオチド配列のうち少なくとも1以上を含むデータセットおよび／または配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178および180で表されるアミノ酸配列のうち少なくとも1以上を含むデータセットを保存したコンピュータ読み込み可能媒体。

29. 請求項28に記載の媒体上のデータと他のヌクレオチド配列および／または他のアミノ酸配列のデータを比較して他のポリヌクレオチド配列および／またはアミノ酸配列との同一性の算出を行う方法。

30. 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179から選択されるヌクレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質。

31. 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質。

要 約 書

NF- κ Bの過剰な活性化または阻害が関与する疾患の診断、治療または予防等に使用されるNF- κ B作用を有するタンパク質の提供する。

ヒト肺線維芽細胞等から作製したcDNAライブラリーから、プラスミドpNF- κ B-Lucを用いて、NF- κ Bを活性化する作用を有するタンパク質をコードするcDNAをクローニングして、そのDNA配列およびそれより推定されるアミノ酸配列を決定した。同タンパク質、これをコードするDNA、同DNAを含有する組換えベクターおよび同組換えベクターを含有する形質転換体は、NF- κ Bの活性化を阻害または促進する物質のスクリーニングに使用される。

図1

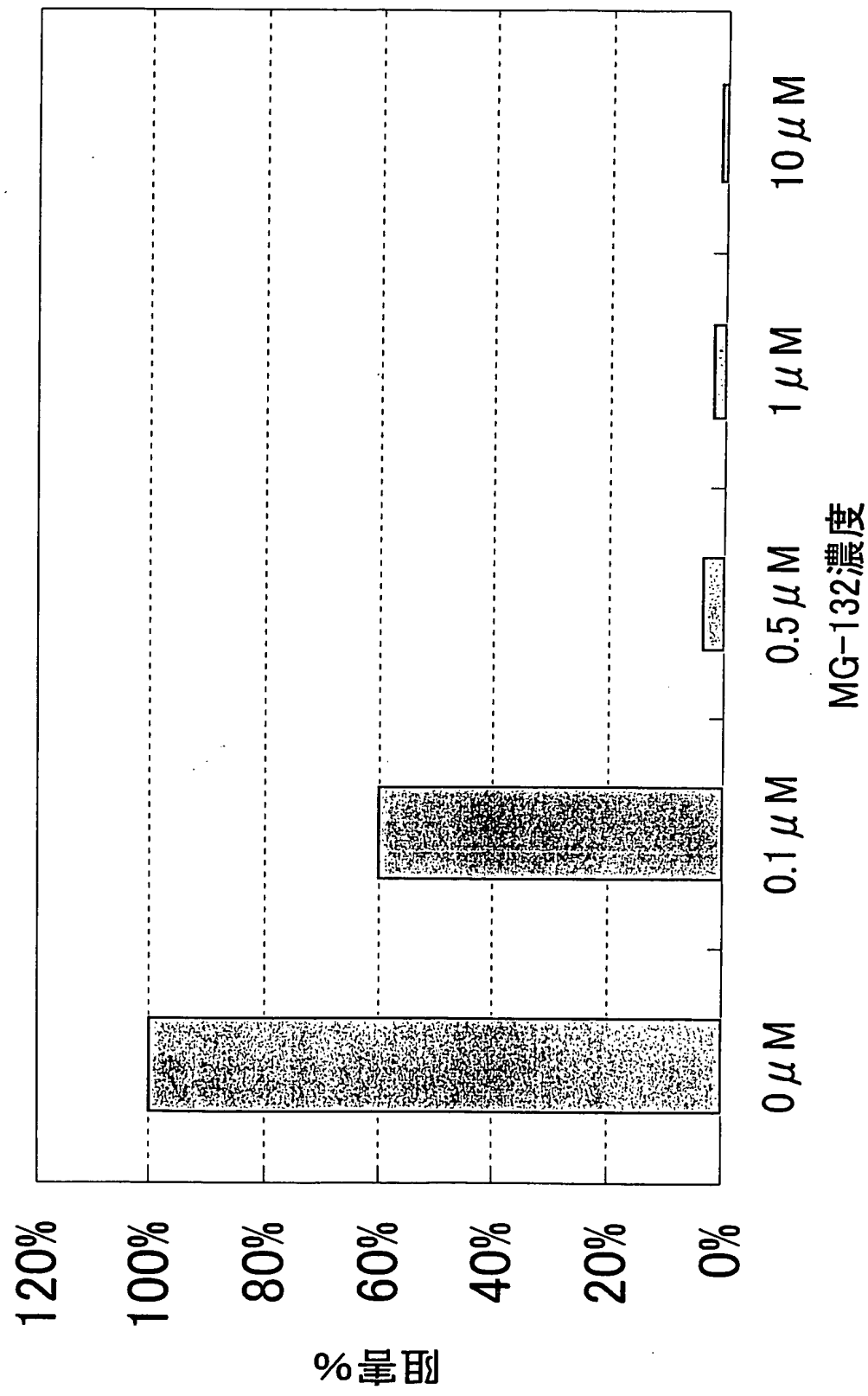


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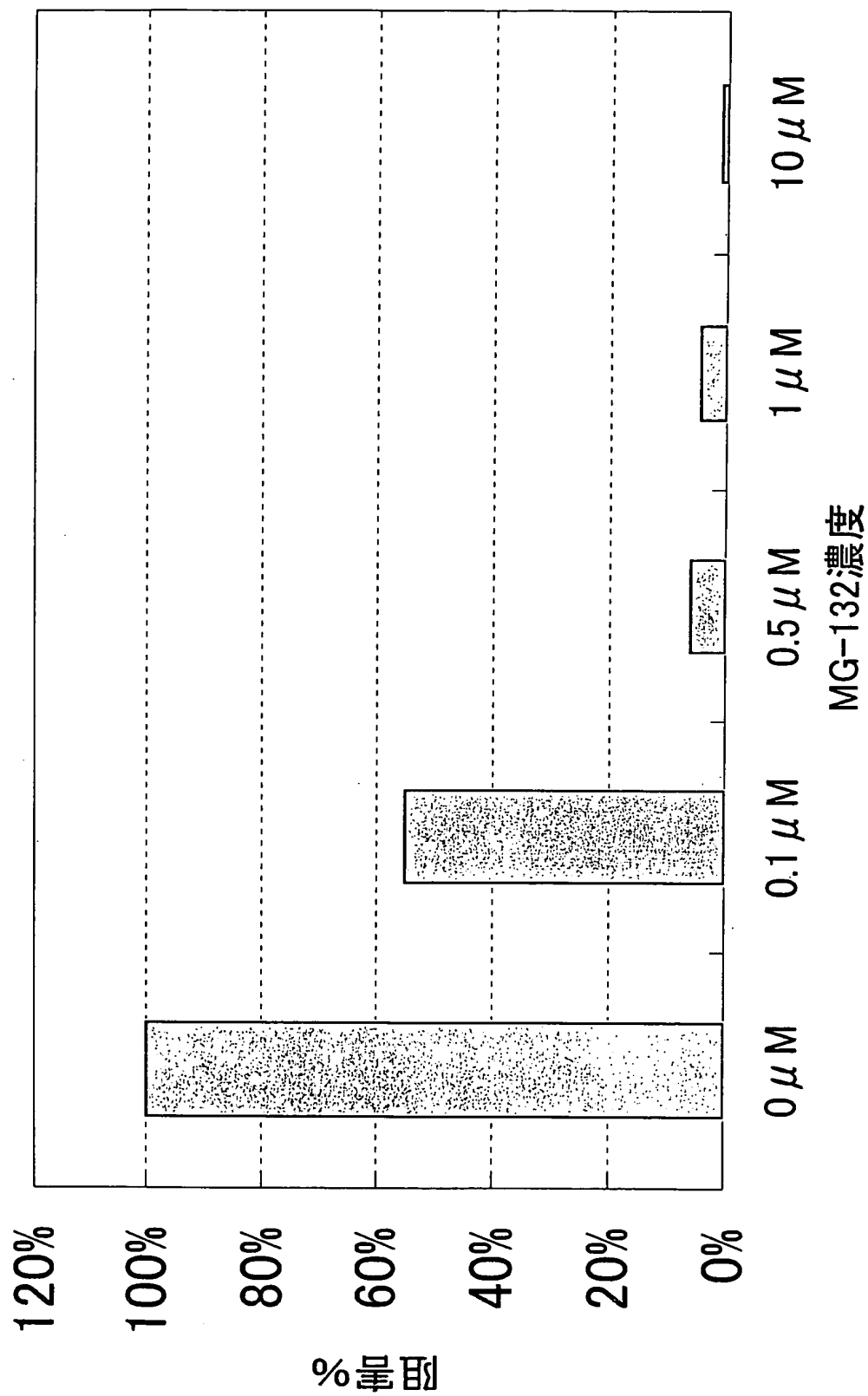


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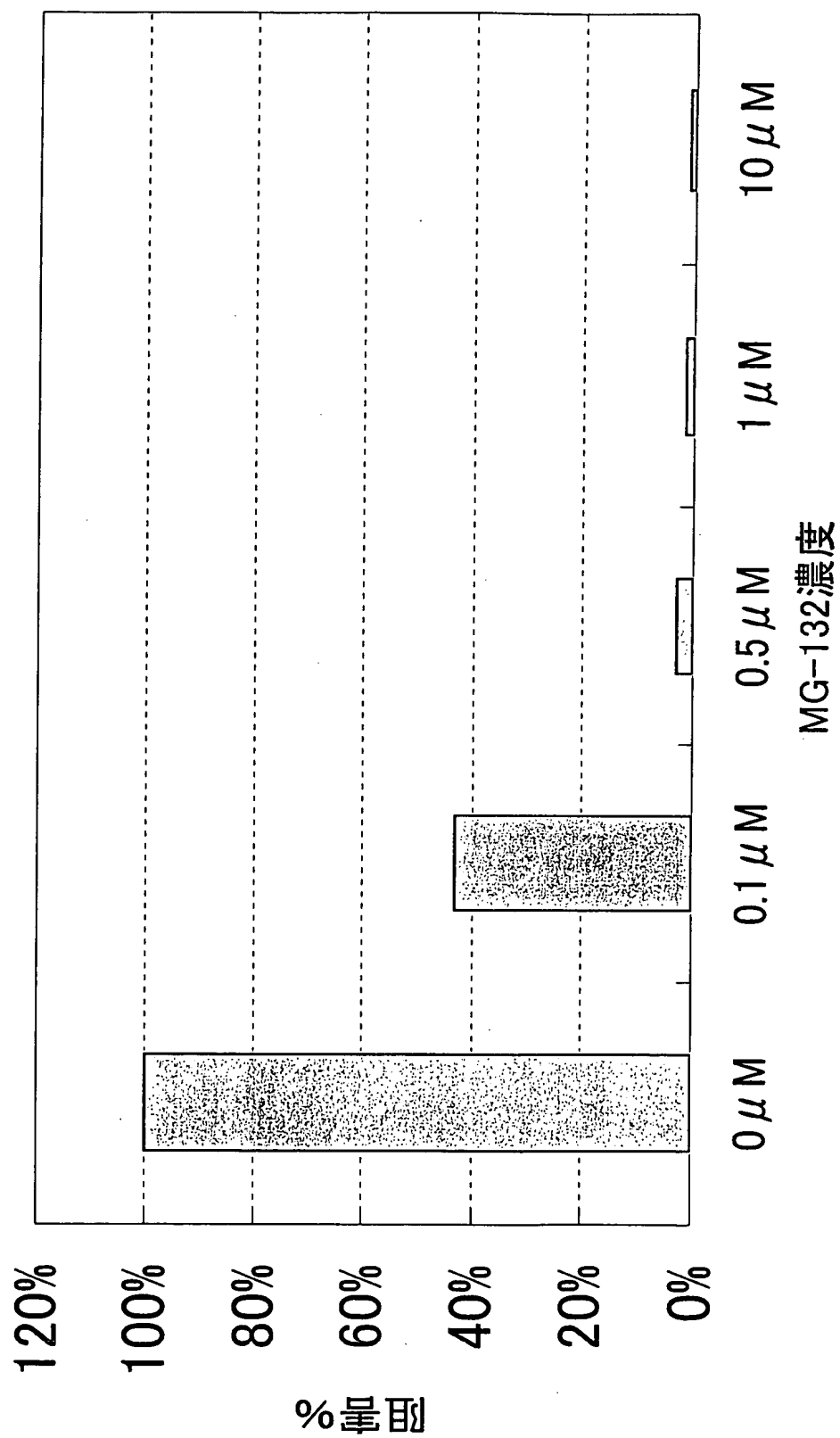


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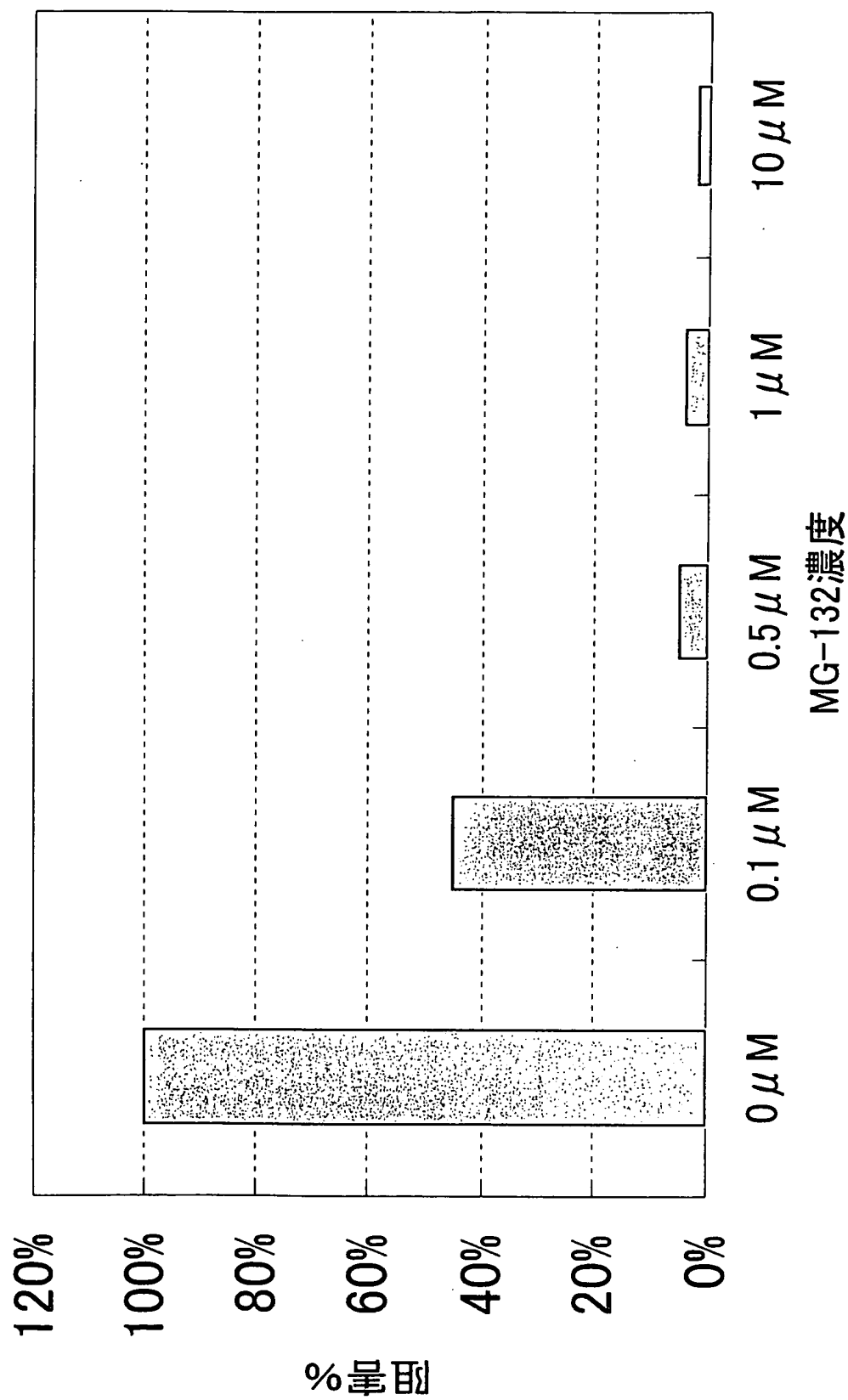


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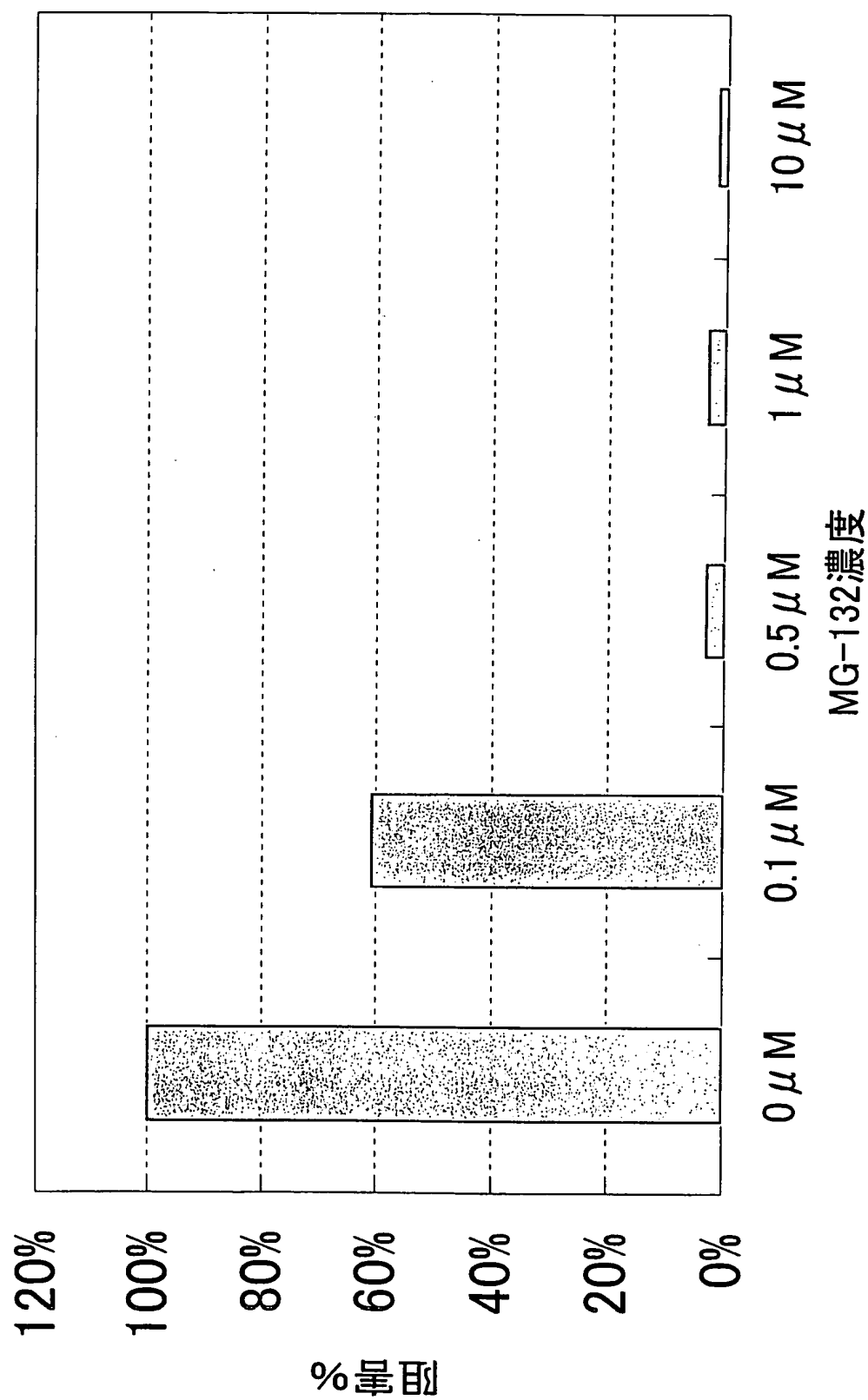


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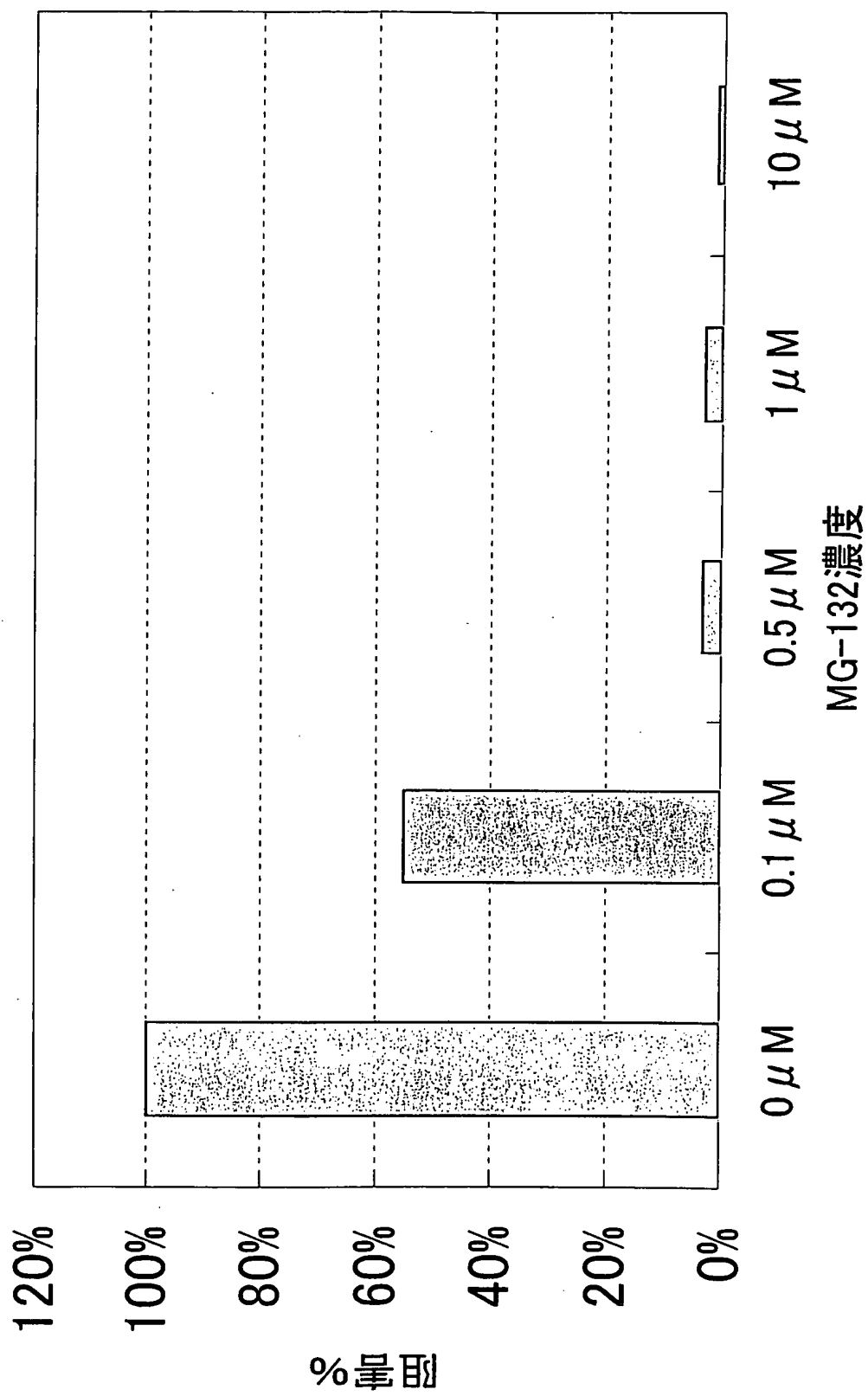


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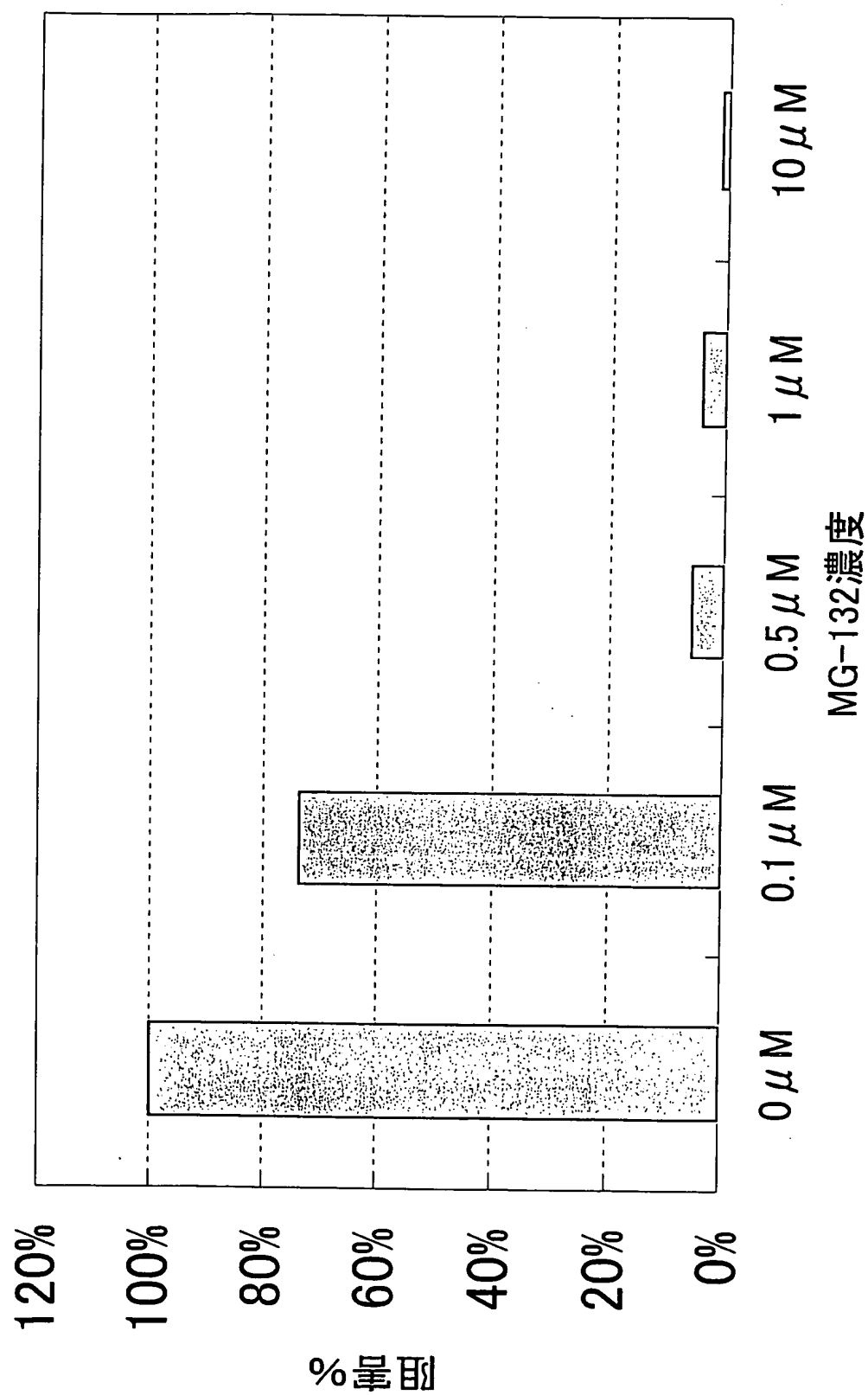


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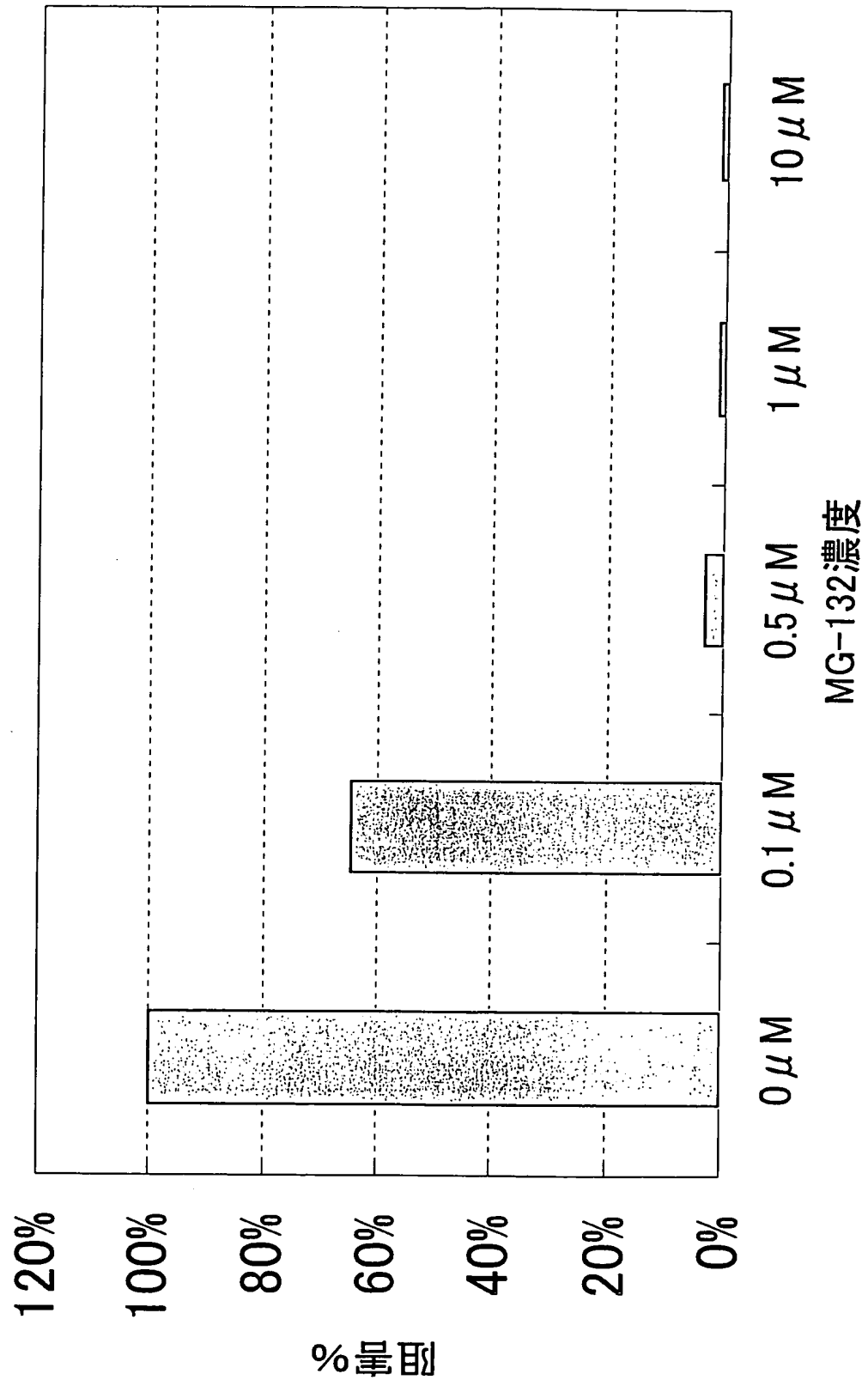


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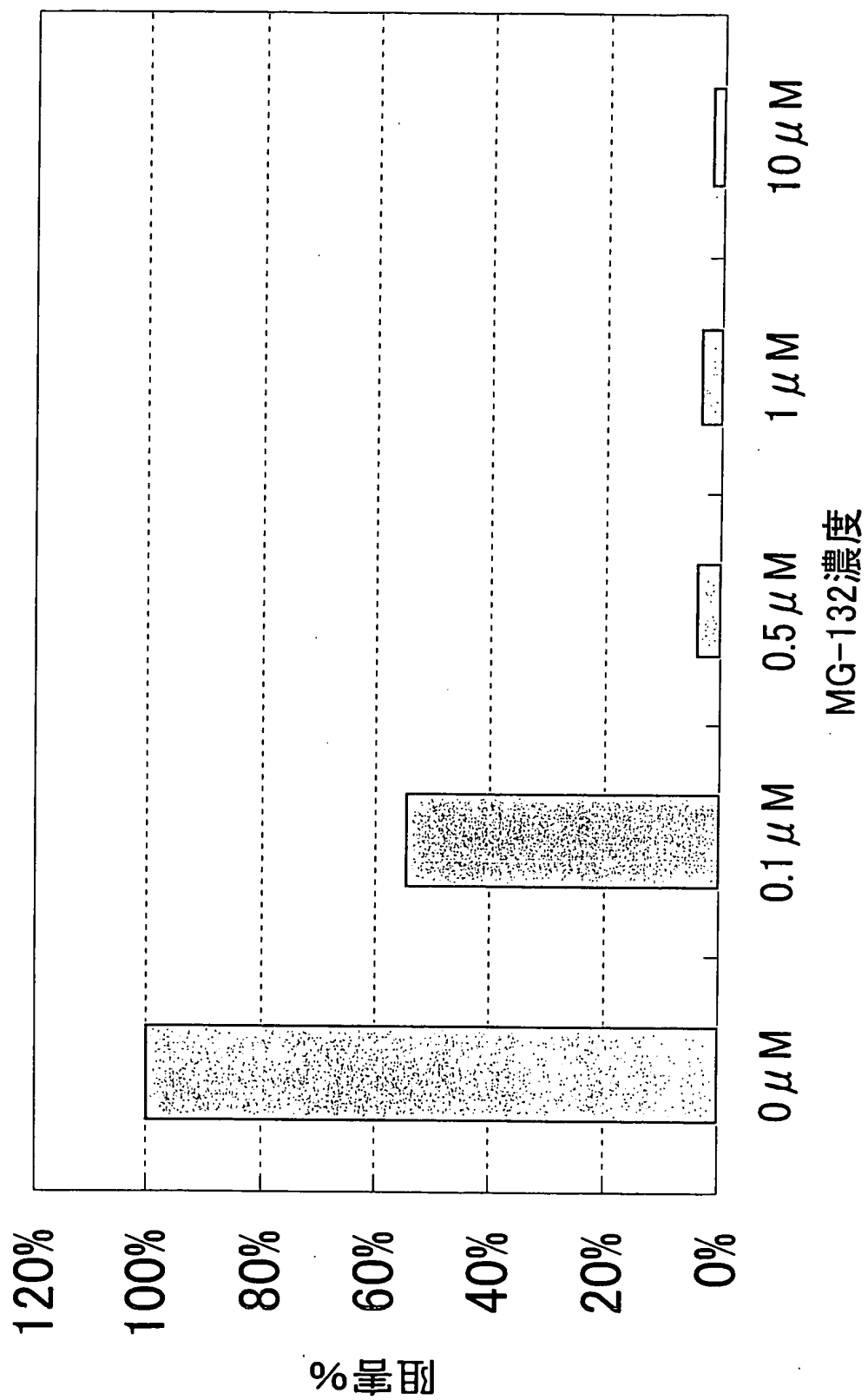


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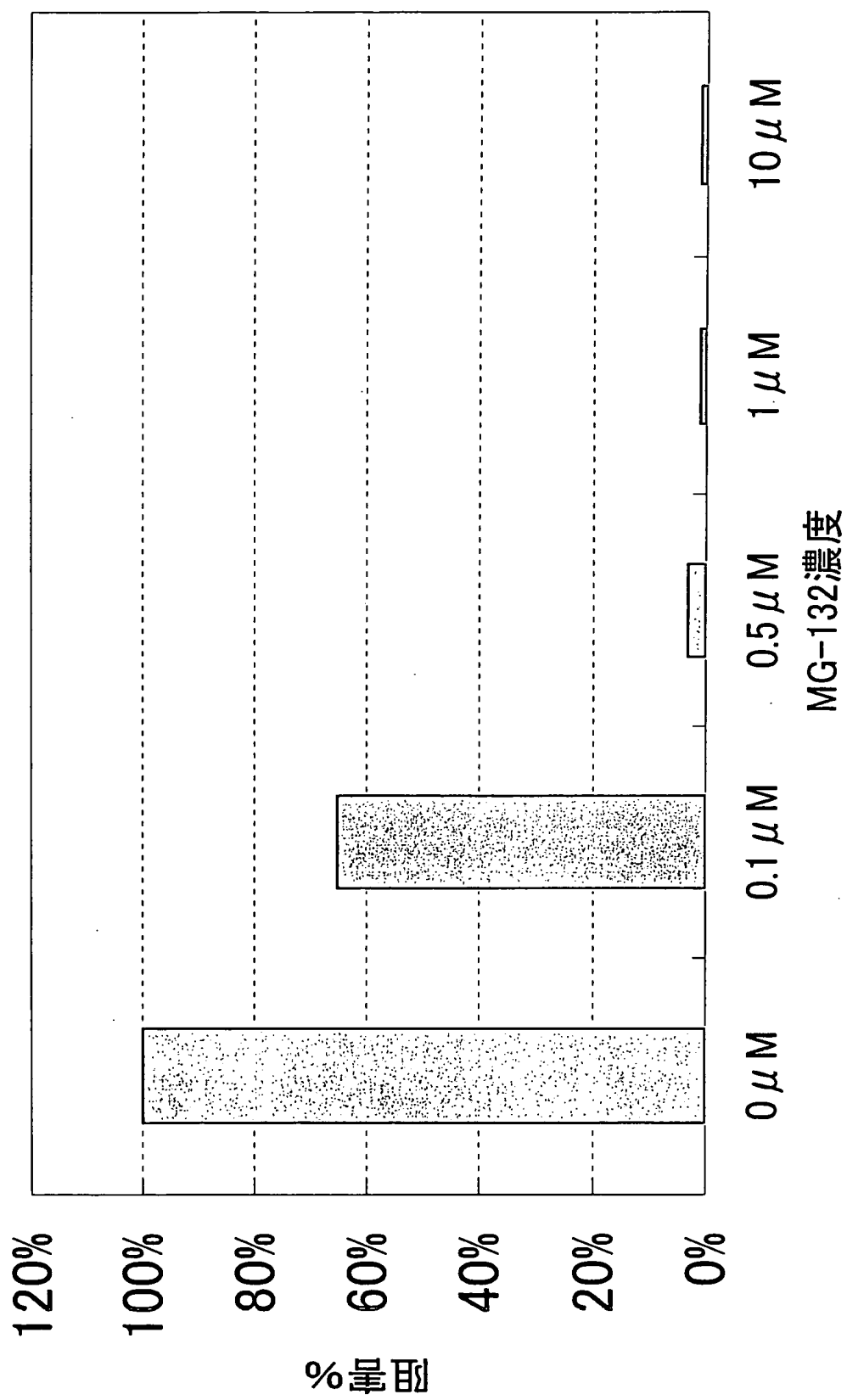


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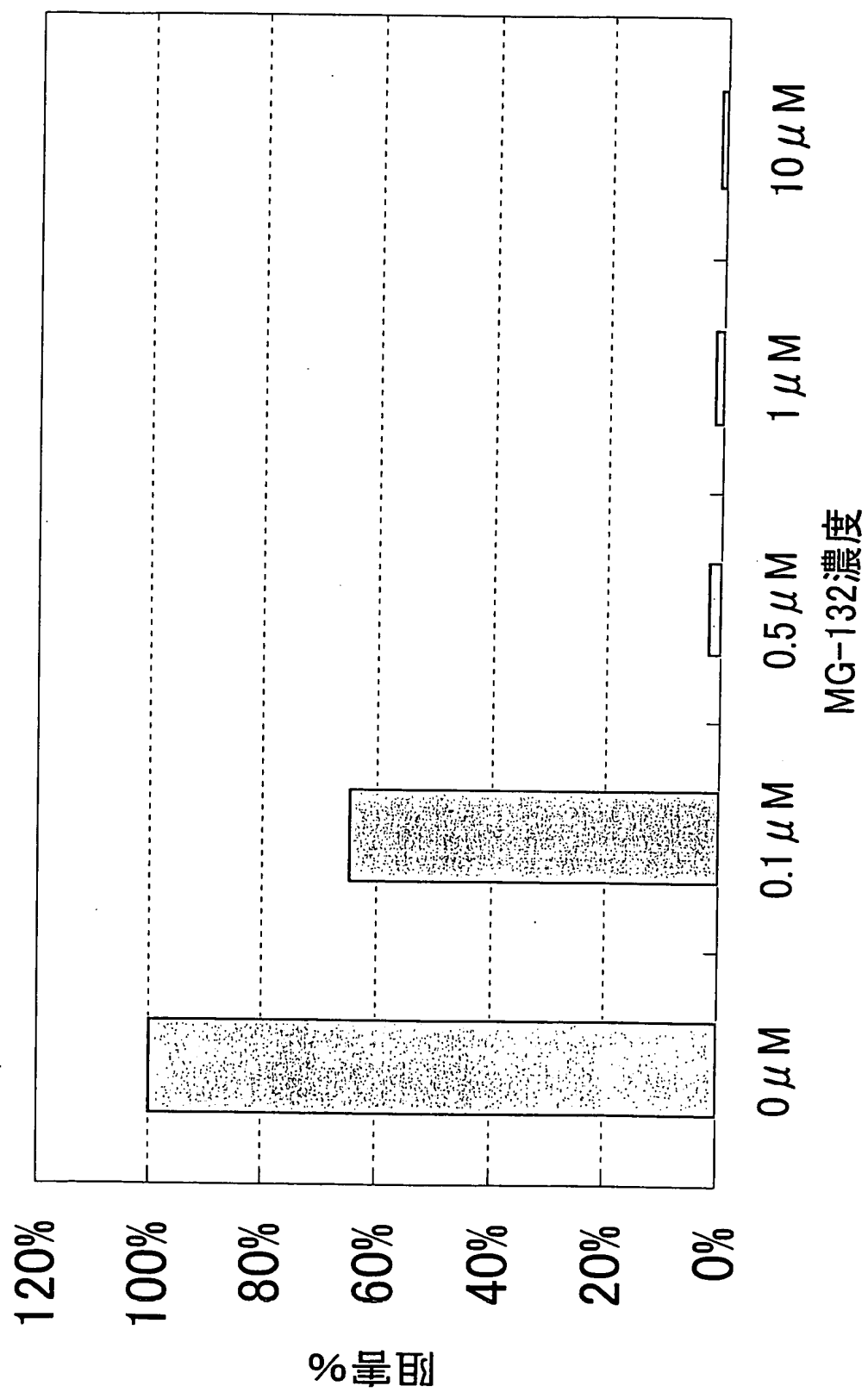


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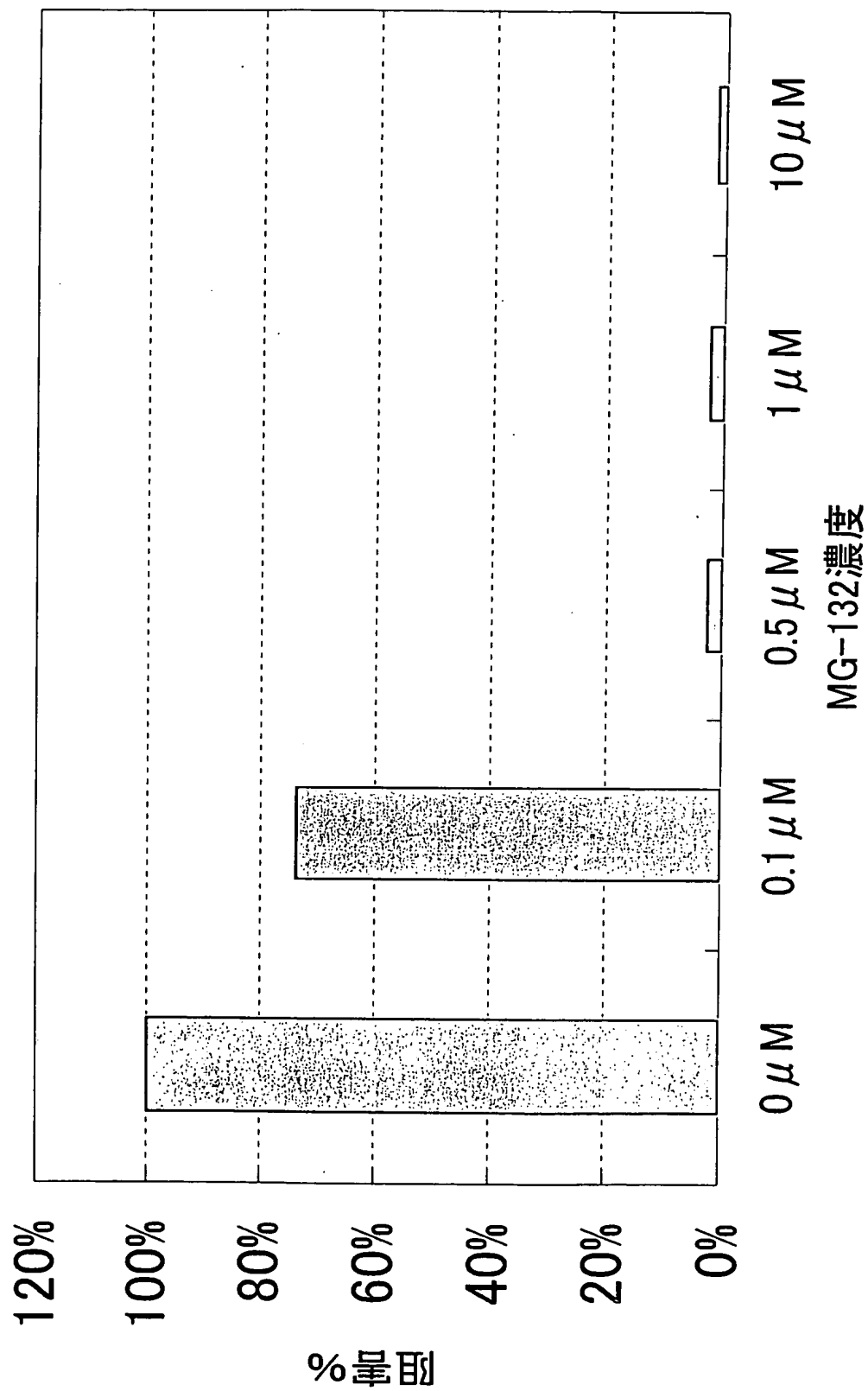


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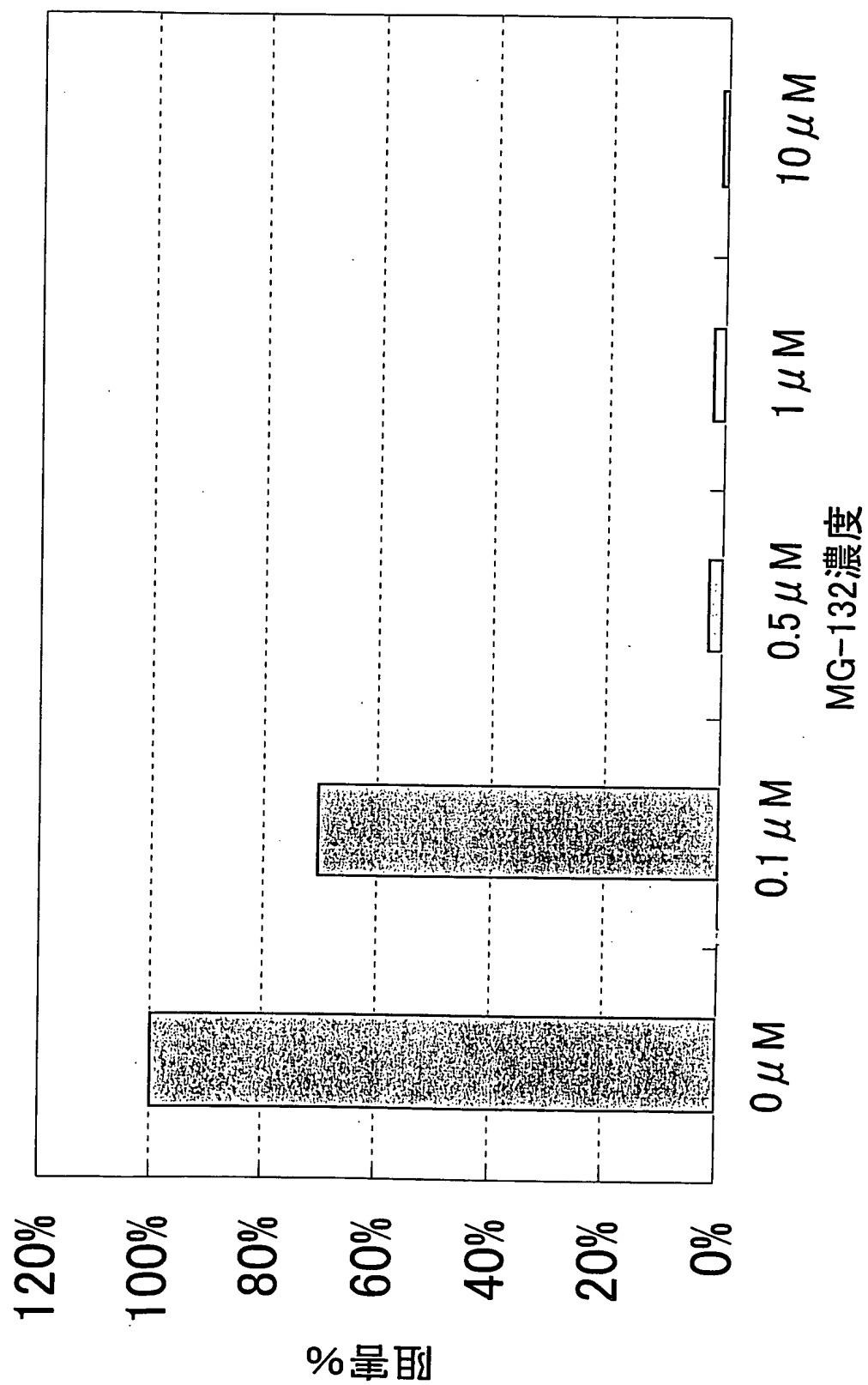


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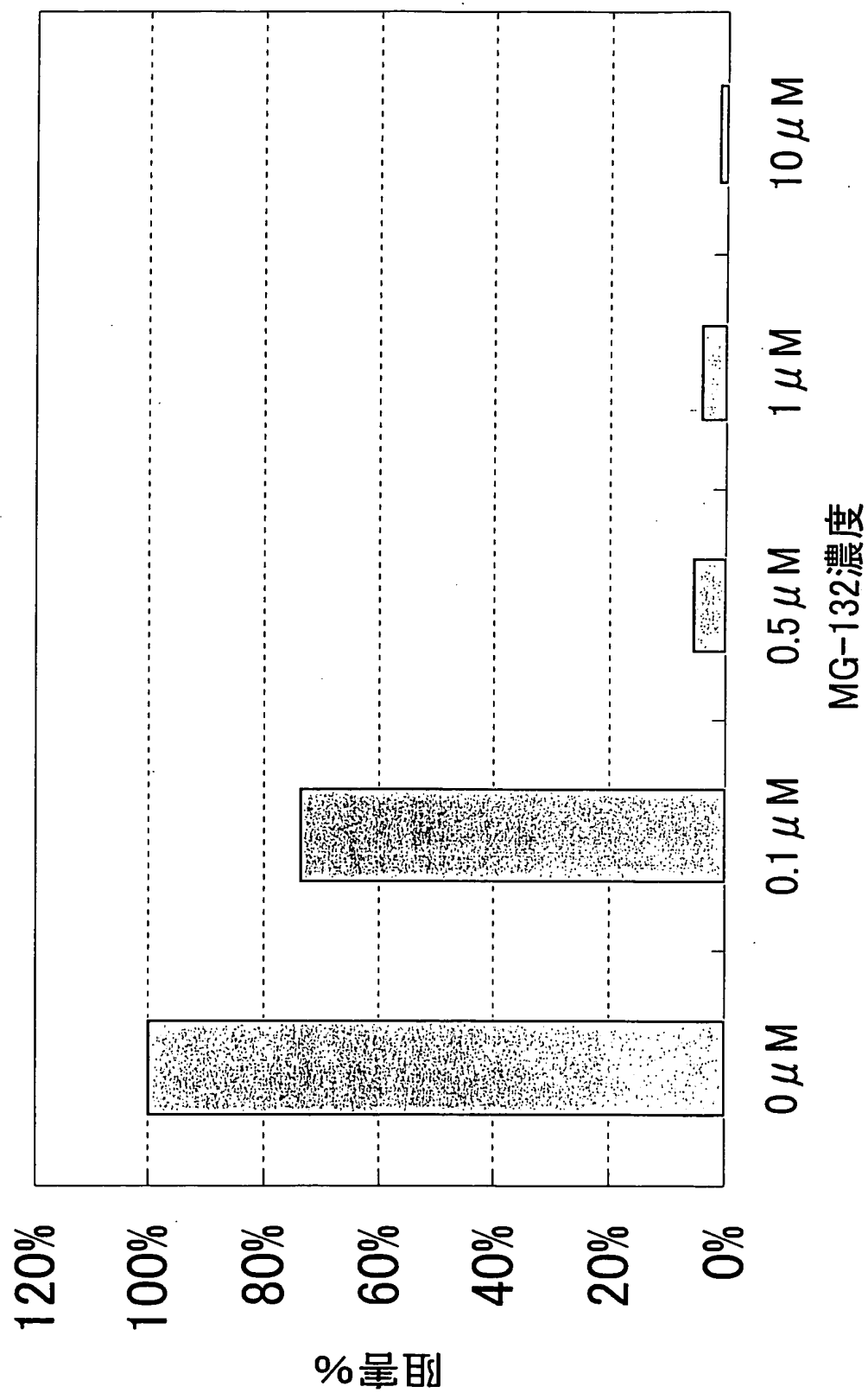


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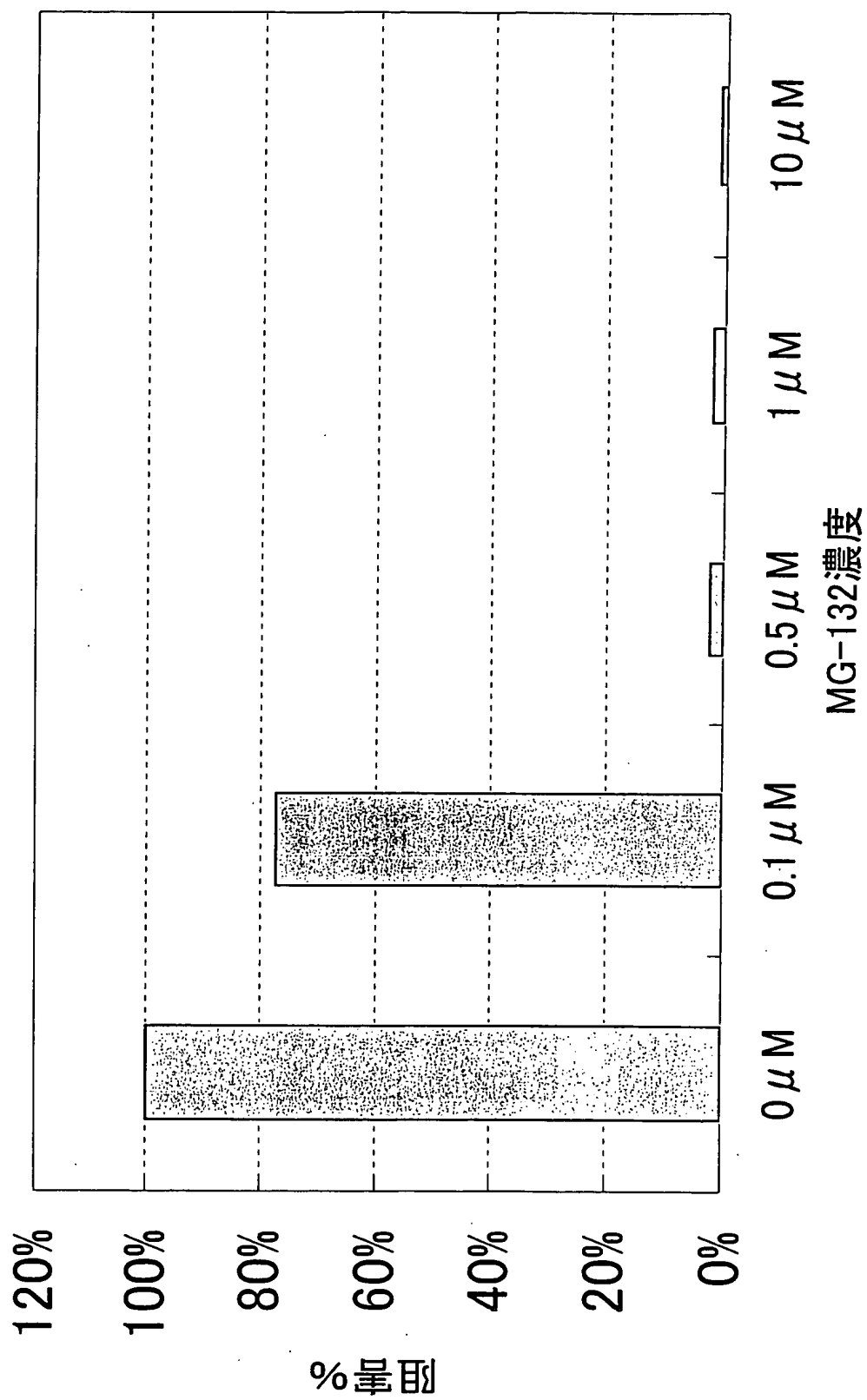


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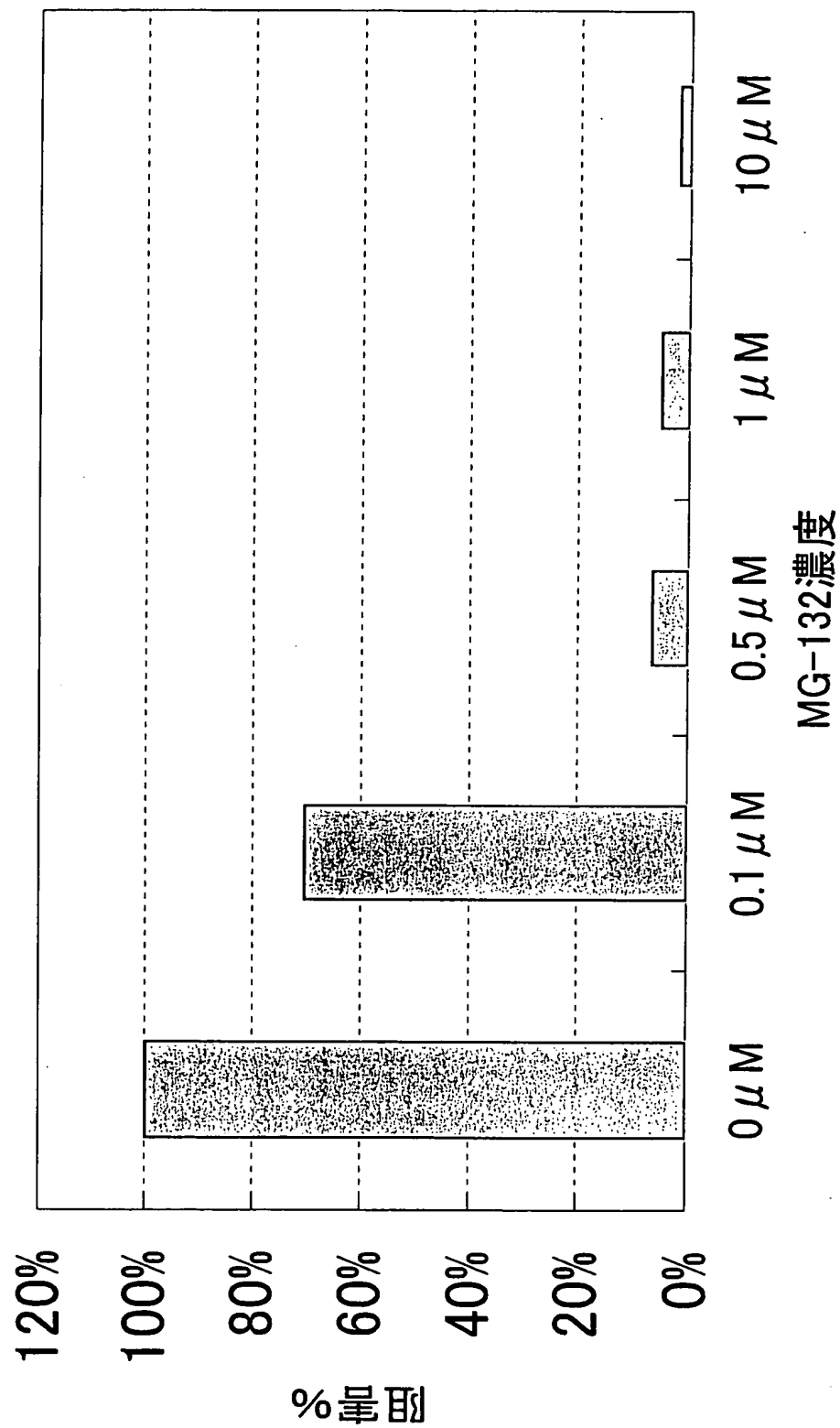


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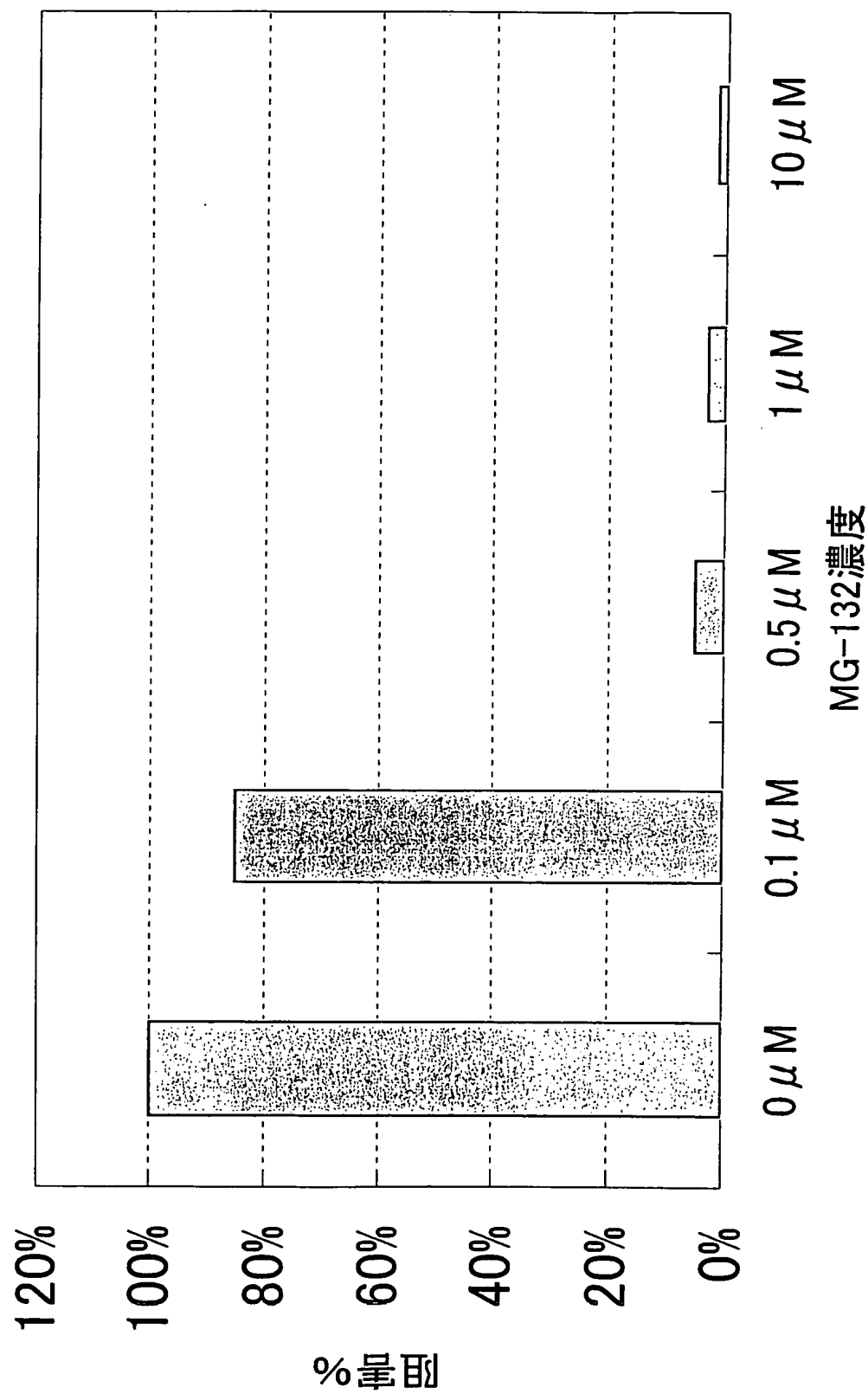


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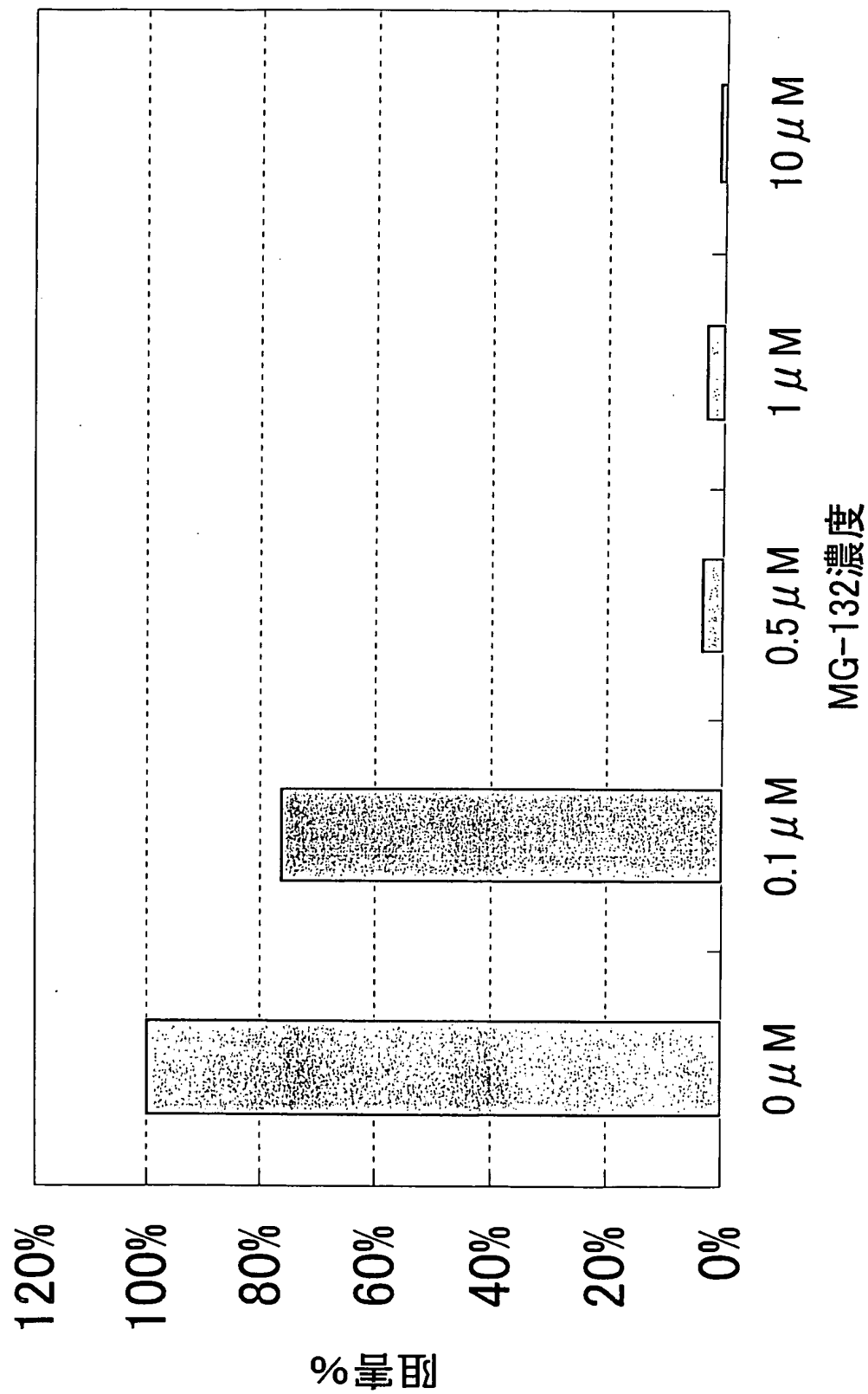


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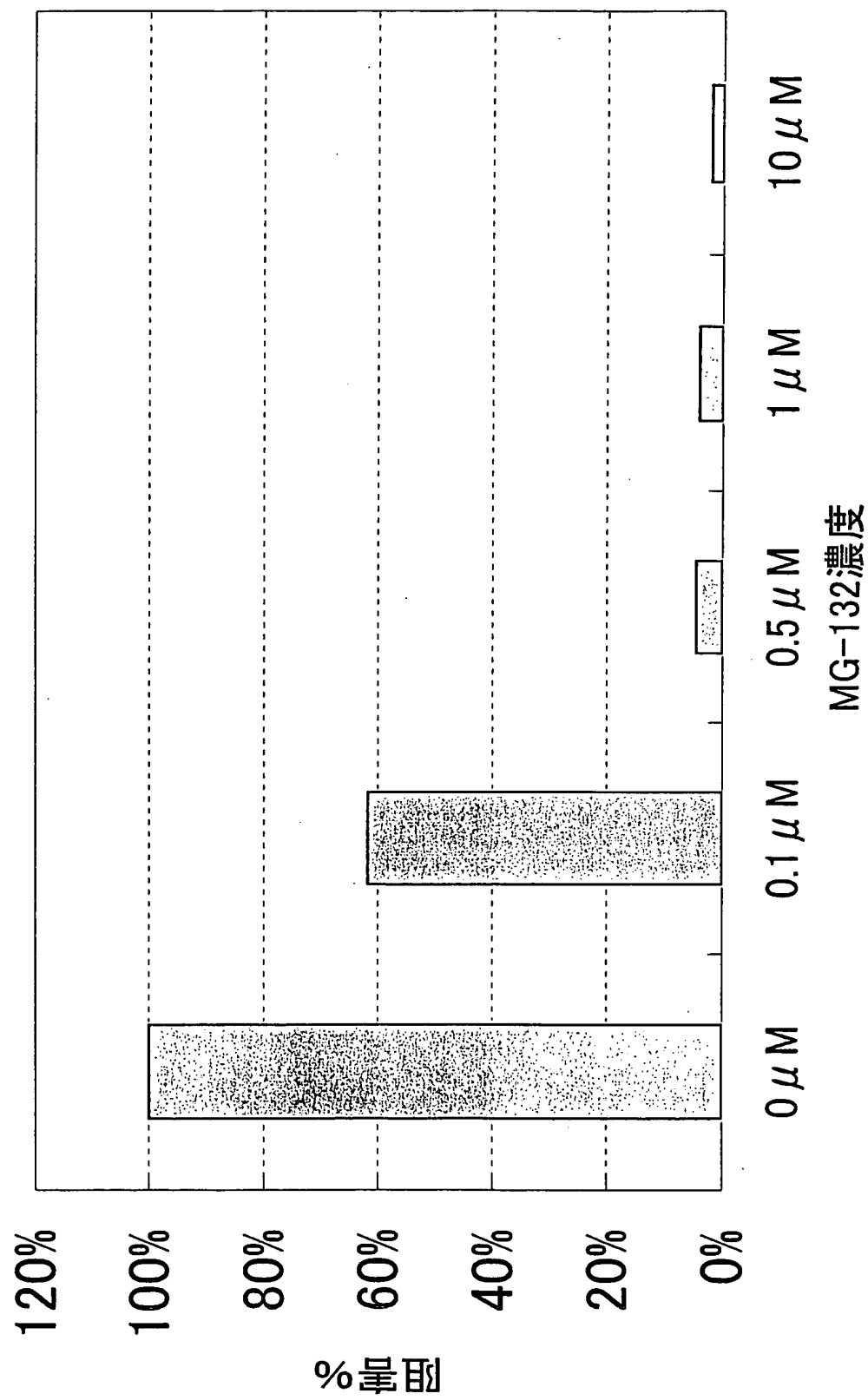


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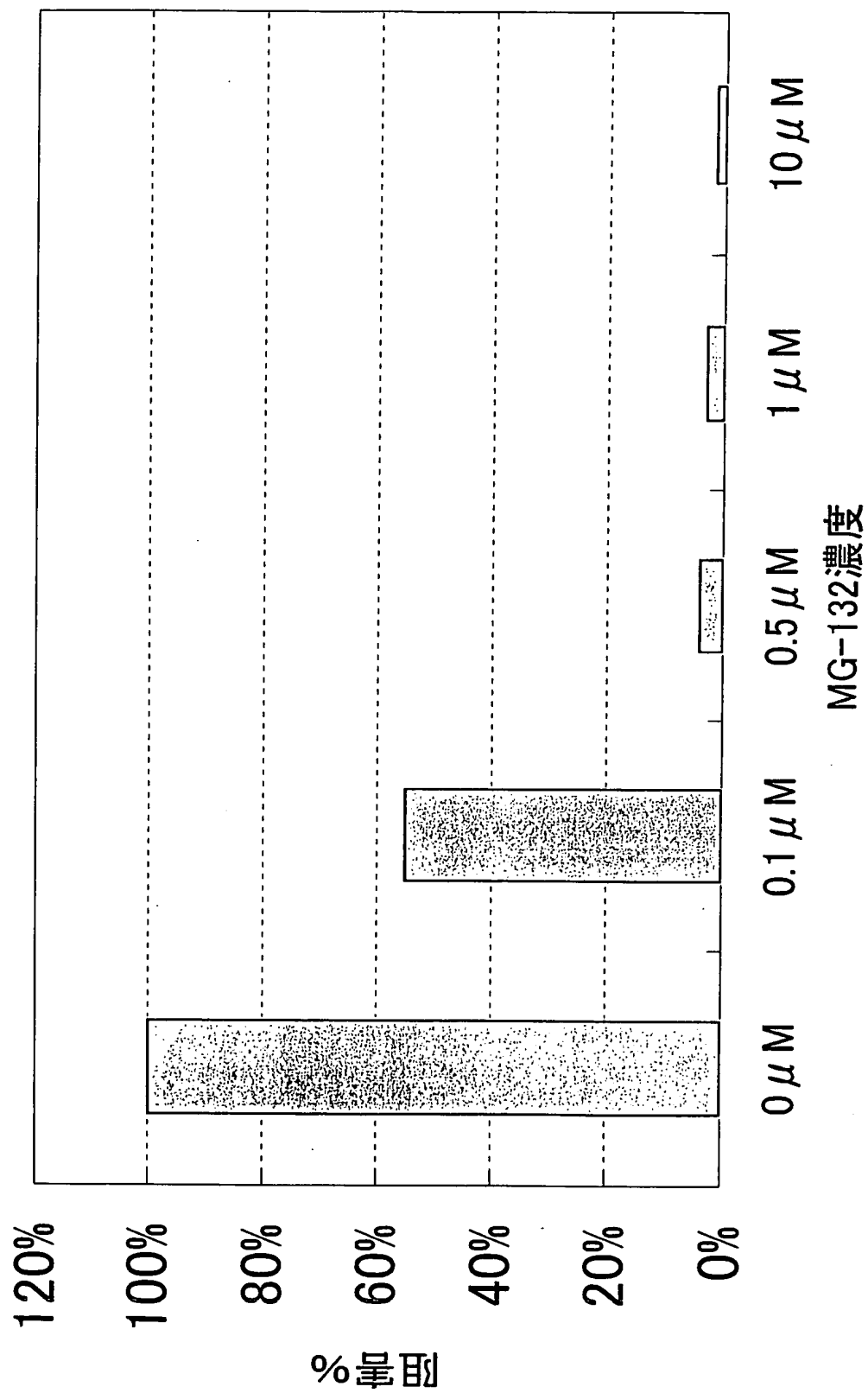


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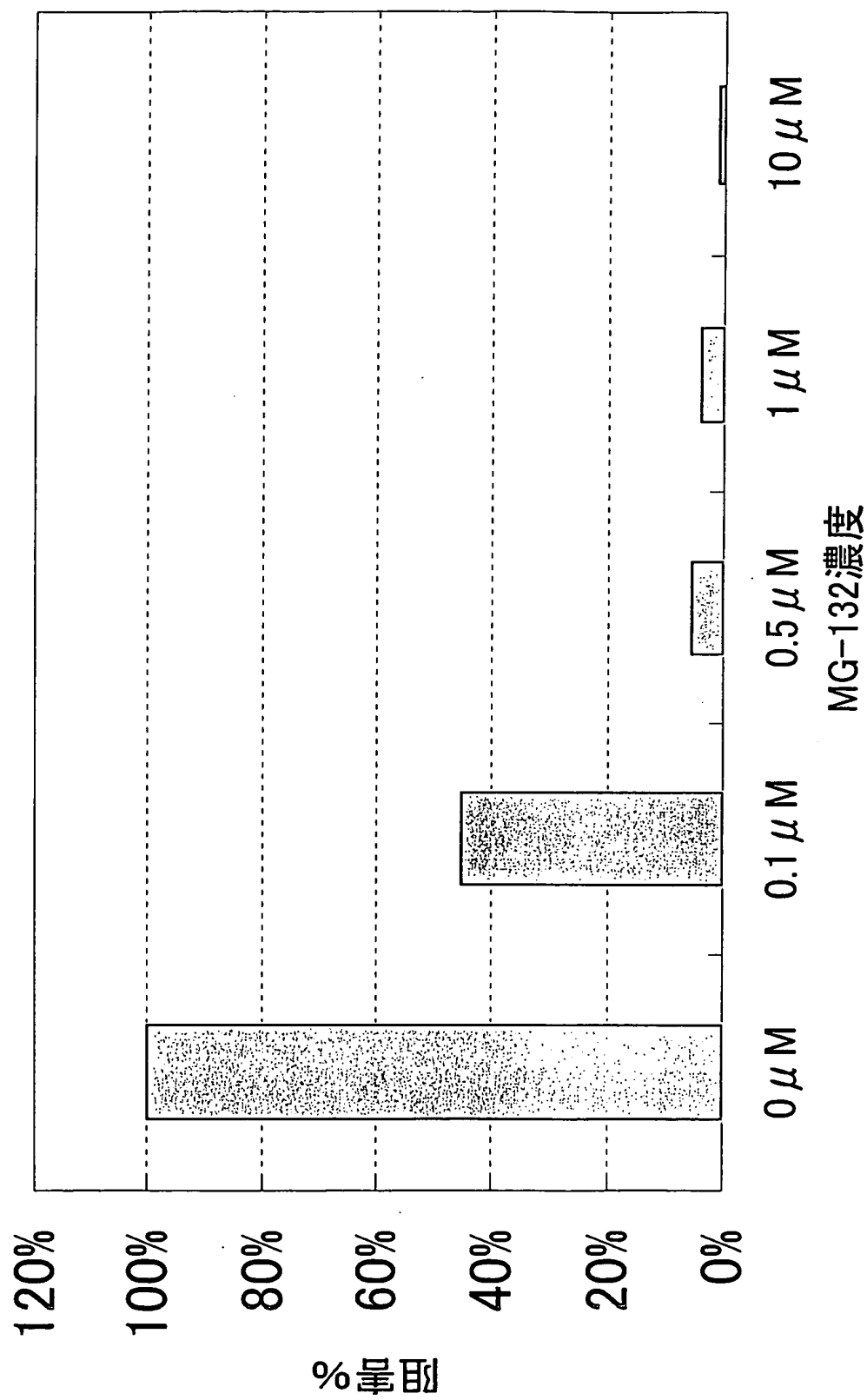


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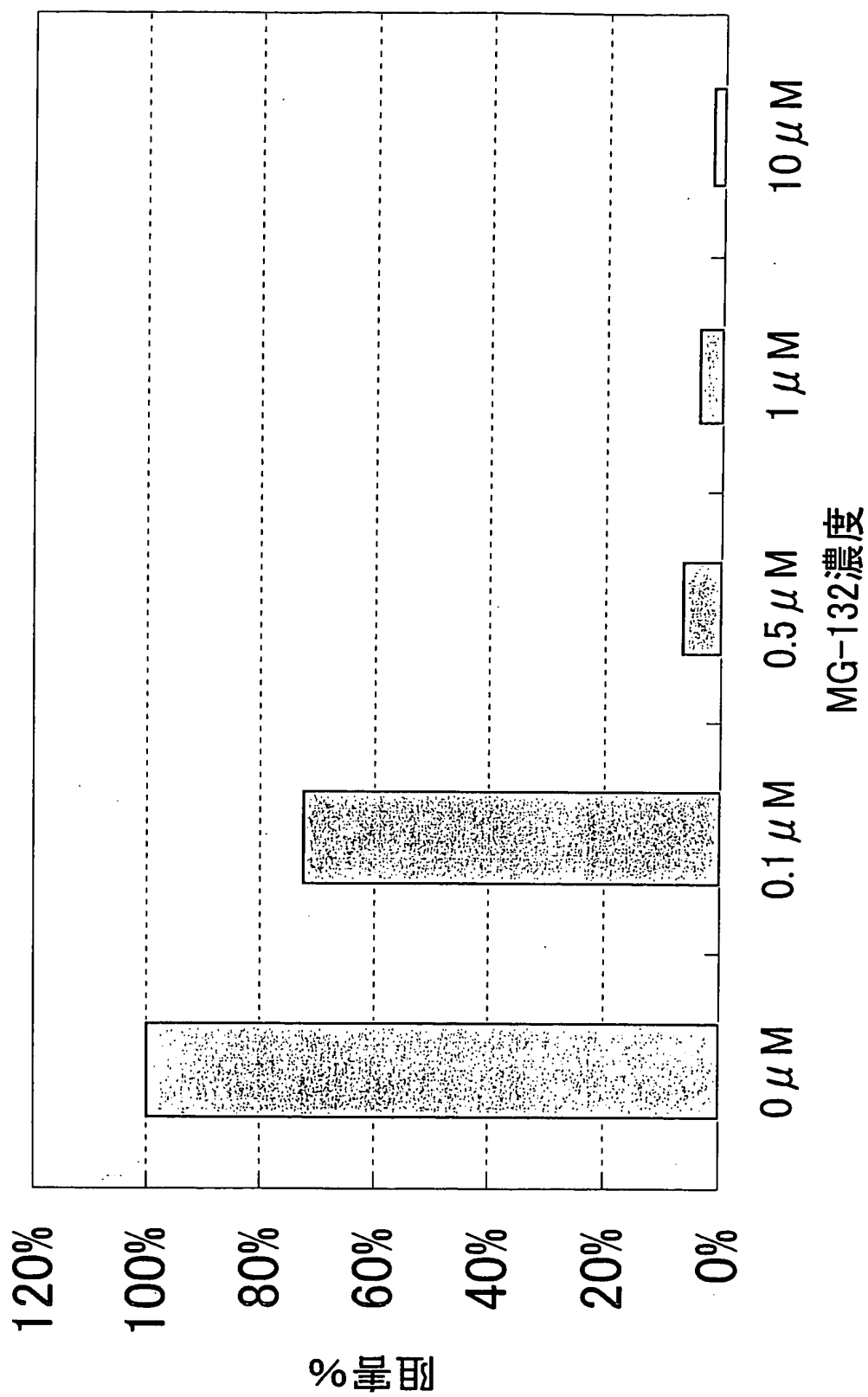


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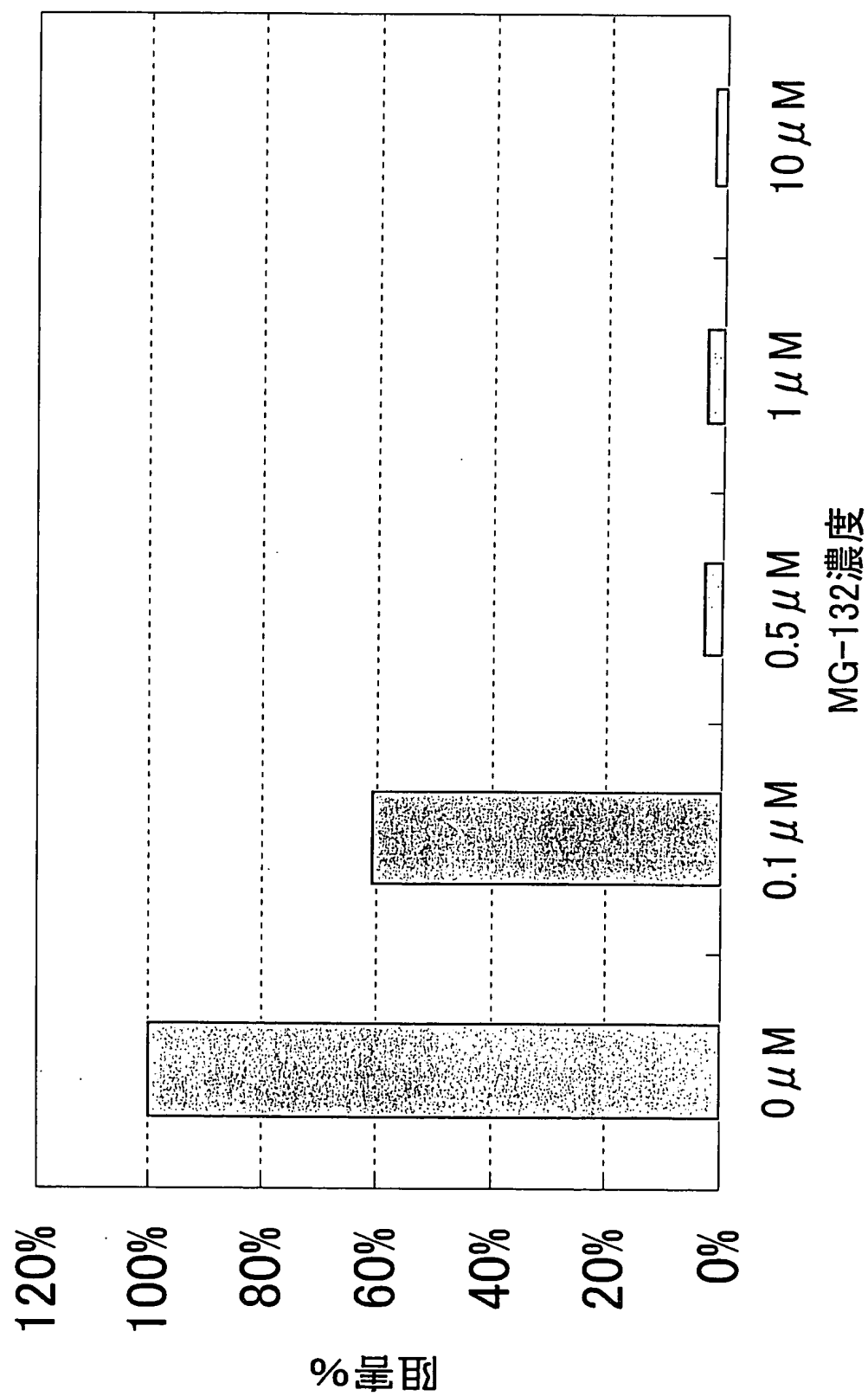


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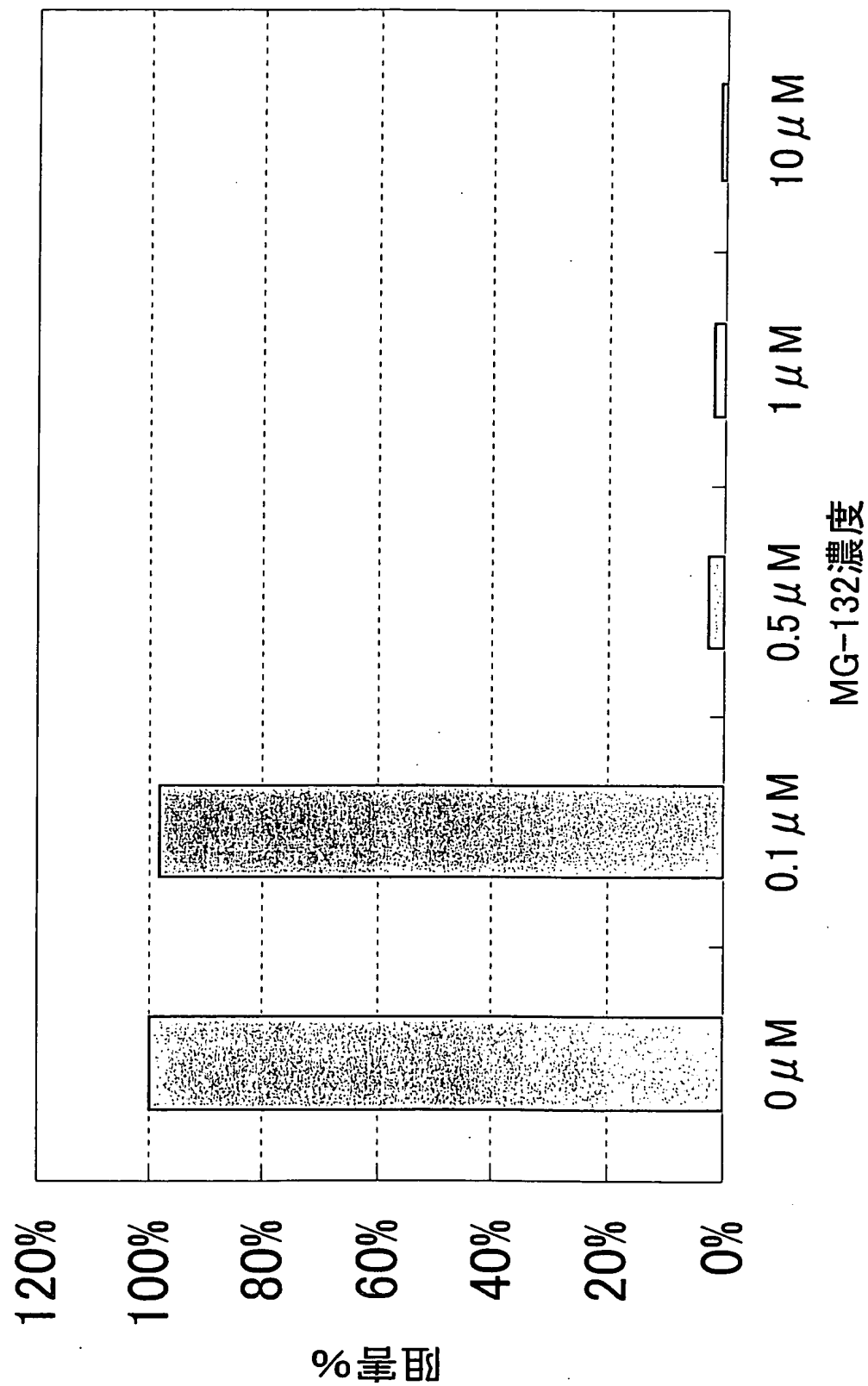


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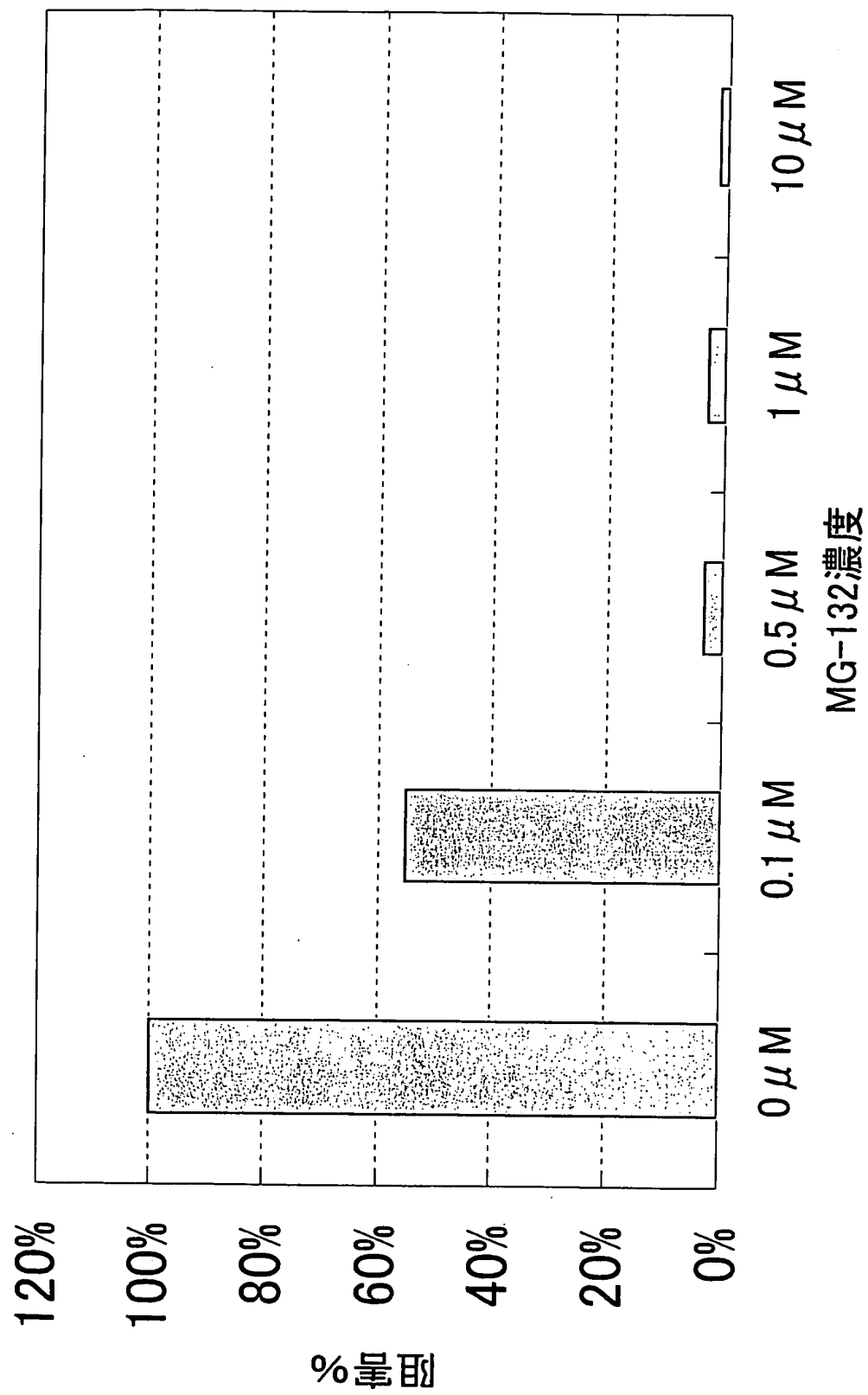


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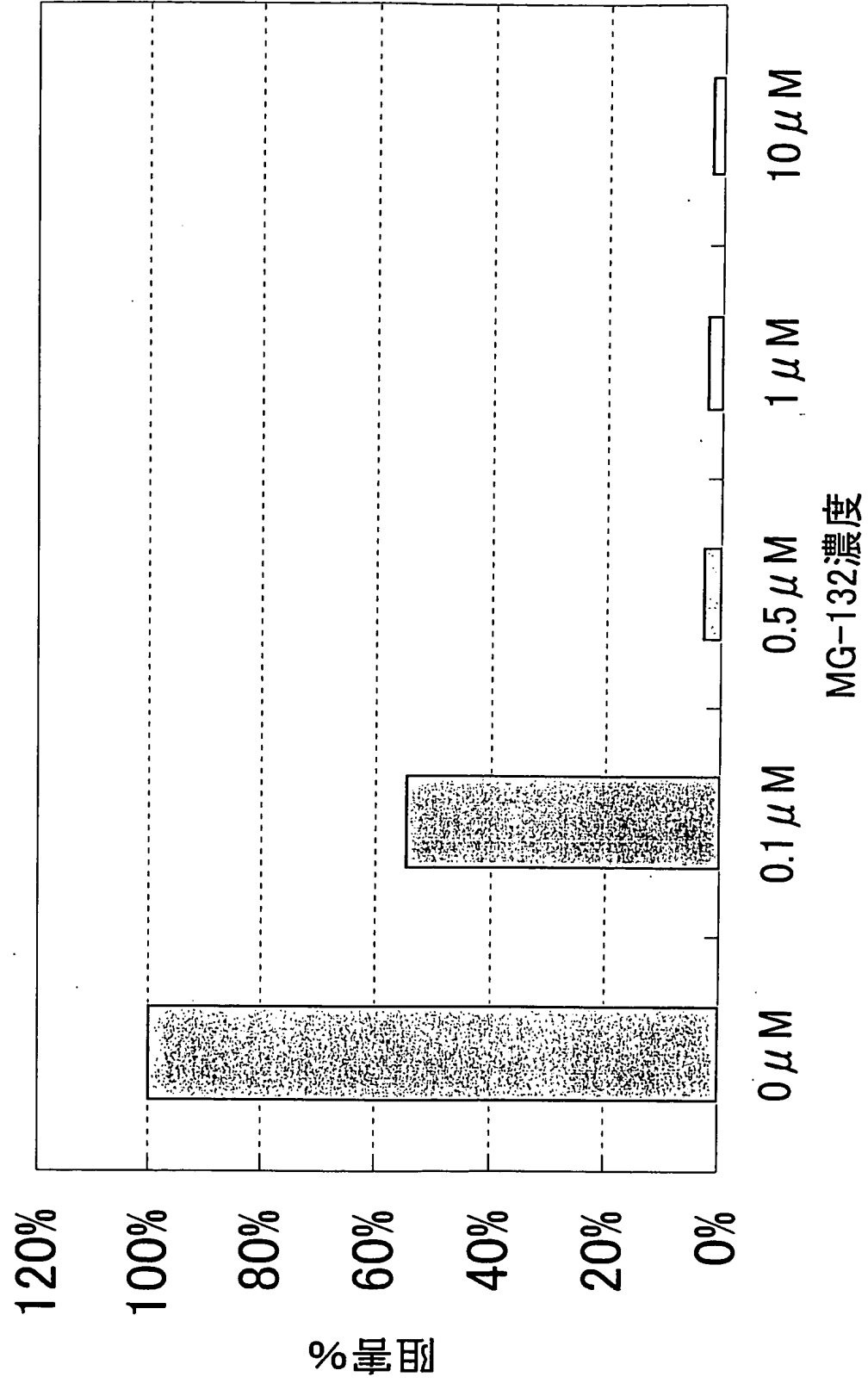


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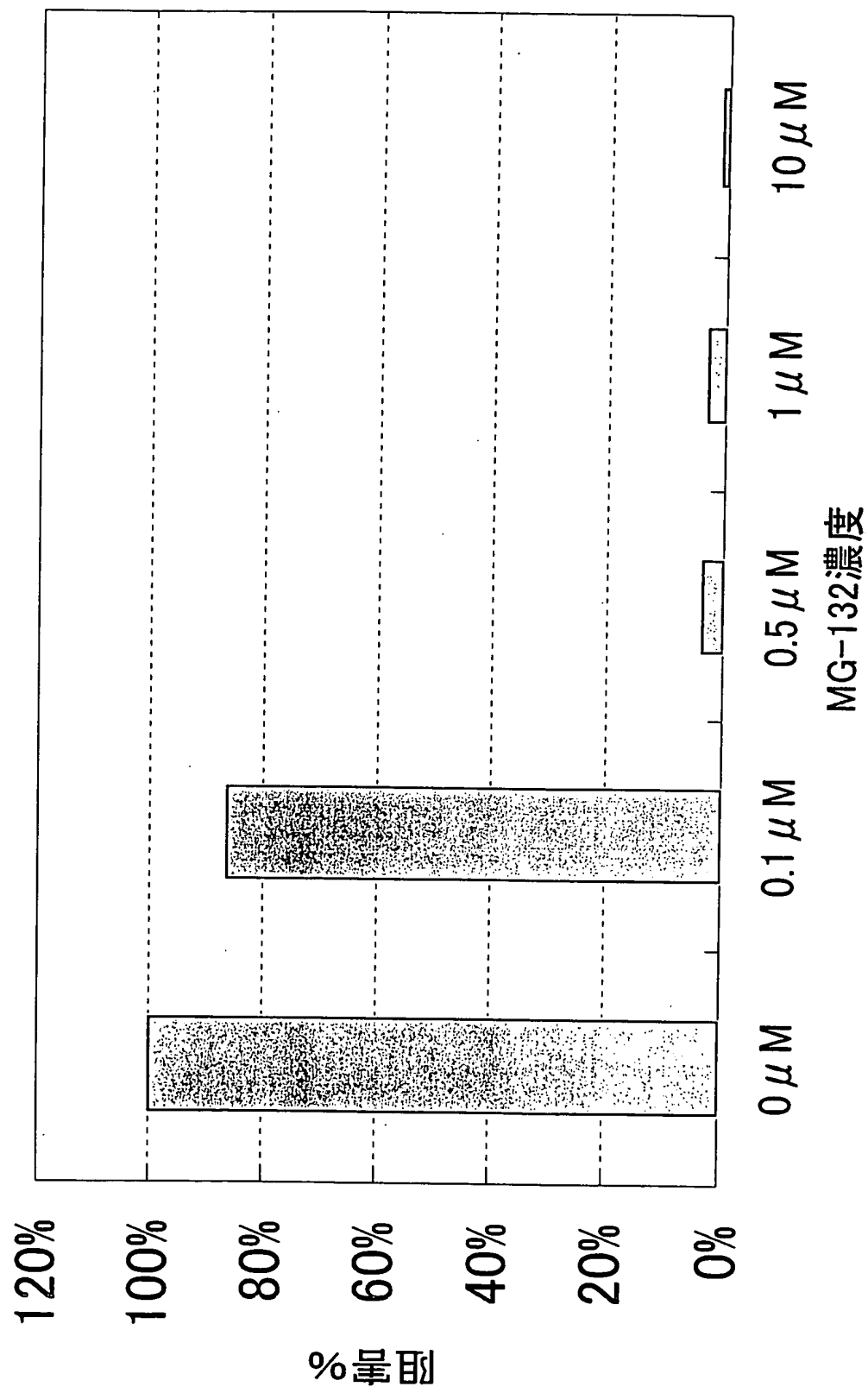


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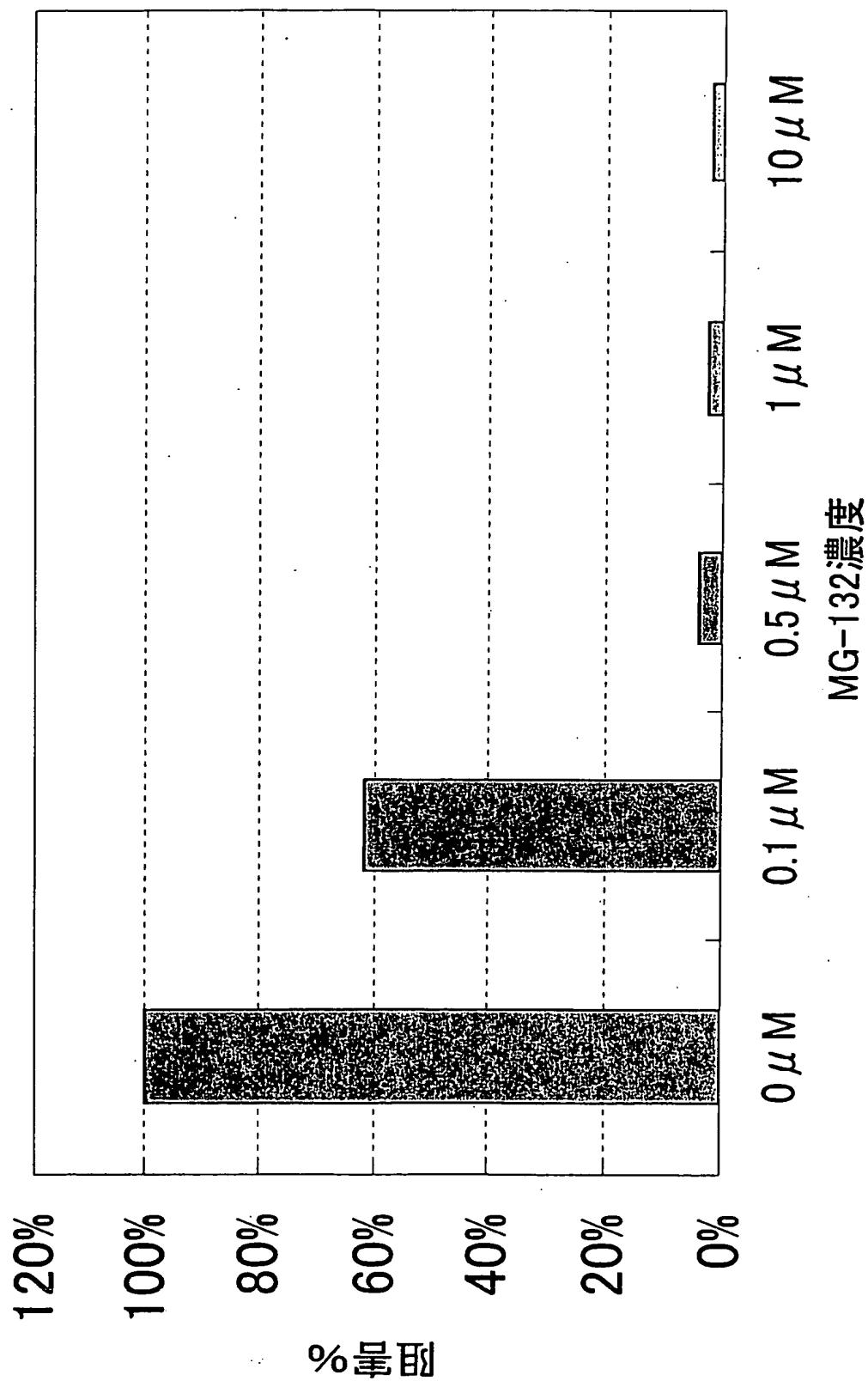
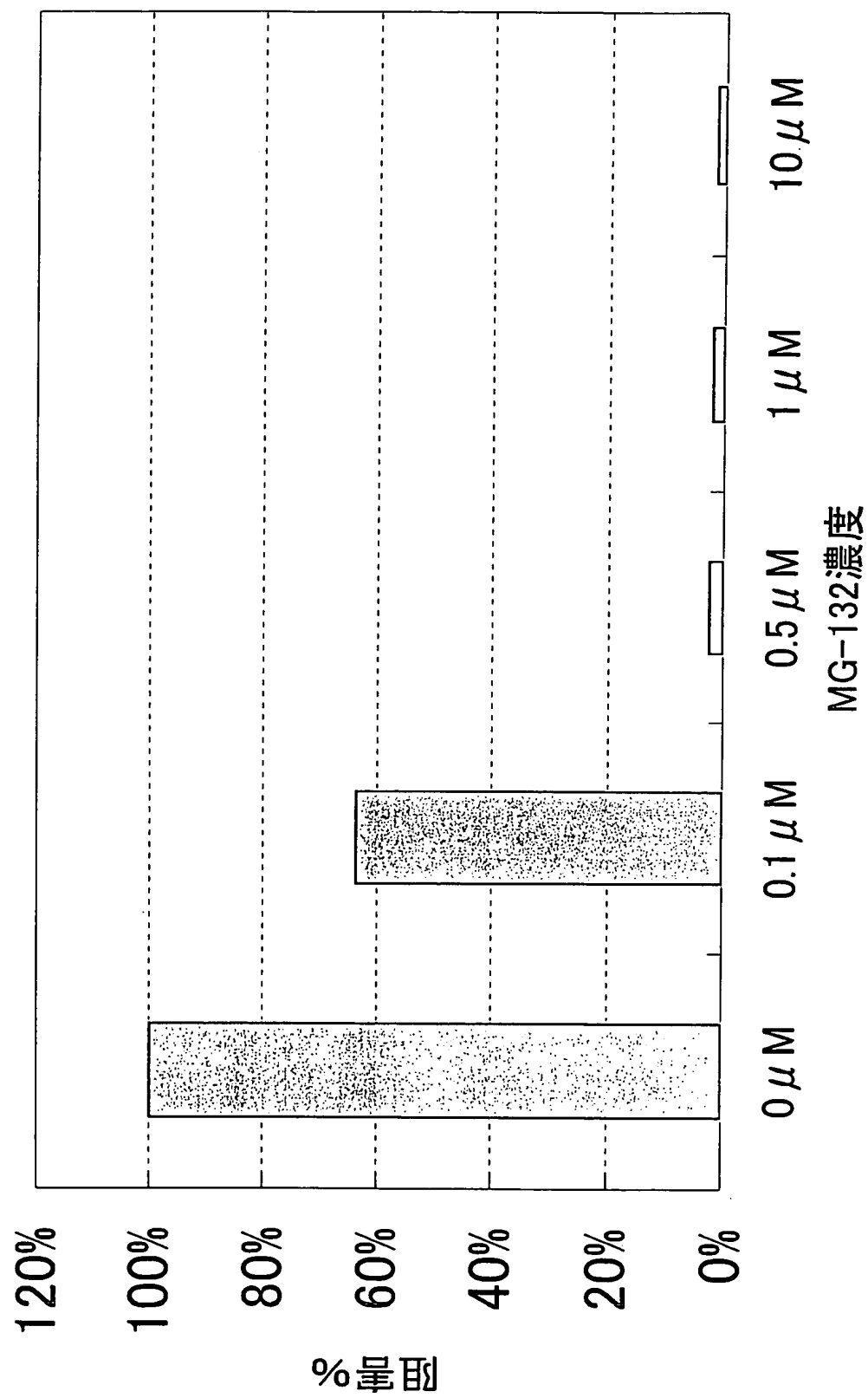


図29



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5

10

atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct 277

Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser

15

20

25

cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325

Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg

30

35

40

ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc 373

Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe

45

50

55

60

aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt 421

Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser

65

70

75

gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg 469

Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp

80

85

90

aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat 517

Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn

95

100

105

aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct 565

Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro

110	115	120	
ccc tcc tac cct ggc acg tgg aat agg gct tac tca ccc ctt cat gga 613			
Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly			
125	130	135	140
ggc tcg ggc agc tat tcg gta tgt tca aac tca gac acg aaa acc aga 661			
Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg			
	145	150	155
act gca tca gga tat ggt ggt acc agg aga cga taaagtagaa agttggagtc 714			
Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg			
	160	165	
aaacactgga tgcagaaatt ttggatTTTT catcactttc tctttagaaa aaaagtacta 774			
cctgttaaca attgggaaaa ggggatattc aaaagttcgg tgggtgtatg tccagtgtag 834			
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tgctggcaaa aatgcttgaa acctctatat ttctttcgtt cataagaggt aaaggtcaaa 1374

tttttcaaca aaagtctttt aataacaaaa gcatgcagtt ctctgtgaaa tctcaaatat 1434

tggttgtaata gtctgtttca atcttaaaaa gaatcaat 1472

<210> 3

<211> 339

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu

1 5 10 15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

20 25 30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35 40 45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50 55 60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65 70 75 80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
85 90 95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
100 105 110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
115 120 125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
130 135 140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145 150 155 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
165 170 175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
180 185 190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
195 200 205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro

210

215

220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His

225

230

235

240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr

245

250

255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile

260

265

270

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp

275

280

285

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn

290

295

300

Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys

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310

315

320

Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr

325

330

335

Arg Arg Arg

<210> 4

<211> 1924

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115)..(1131)

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cccaggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg 117

Met

1

gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165

Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly

5

10

15

ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213

Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp

20

25

30

cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261

Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr

35

40

45

gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309

Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys

50

55

60

65

tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile

70 75 80

cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys

85 90 95

aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser

100 105 110

tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser

115 120 125

tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549
 Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys

130 135 140 145

ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597
 Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr

150 155 160

tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile

165 170 175

acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693
 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
 180 185 190

ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741
 Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
 195 200 205

ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789
 Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
 210 215 220 225

cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837
 Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
 230 235 240

gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
 Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
 245 250 255

aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
 Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu
 260 265 270

gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981
 Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
 275 280 285

tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029

Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
 290 295 300 305

gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077
 Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
 310 315 320

aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125
 Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
 325 330 335

aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt 1181
 Arg Arg

catcactttc tctttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc 1241

aaaagttcgg tgggtttatg tccagtgtag ctttttgtat tctattattt gaggctaaaa 1301

gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattg 1361

cagtttttga aagtgatcat tactgtggaa tgctaaaaat acattaattt ctaaaacctg 1421

tgatgcccta agaagcatta agaatgaagg tgttgtacta atagaaacta agtacagaaa 1481

atttcagttt taggtggtg tagctgatga gttattacct catagagact gtaatattct 1541

atttggtatt atattatttg atgtttgctg ttcttcaaac atttaaataca agctttggac 1601

taattatgct aatttgtgag ttctgatcac ttttgagctc tgaagctttg aatcattcag 1661

tggtggagat ggccttctgg taactgaata ttaccttctg taggaaaagg tggaaaataa 1721

gcatctagaa ggttggttg aatgactctg tgctggcaaa aatgcttgaa acctctatat 1781

ttctttcgtt cataagaggt aaaggtcaaa tttttcaaca aaagtctttt aataacaaaa 1841

gcatgcagtt ctctgtgaaa tctcaaatat tgttgtaata gtctgtttca atcttaaaaa 1901

gaatcaataa aaacaaacaa ggg 1924

<210> 5

<211> 127

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1 5 10 15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
115 120 125

<210> 6

<211> 702

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(605)

<400> 6

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ggcgtcttcc gtcccgttcc catcctcgcc gcgctccagc acctctgaag ttttcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacatttta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5 10 15 20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25 30 35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40 45 50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70 75 80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85 90 95 100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572

Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

105

110

115

gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctctctcat 625

Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser

120

125

ccctttcttc cctttgagca ttgccctctt tgggttcttt ttgagccaat tctaataaaa 685

gtaaaaatgg taatagt

702

<210> 7

<211> 233

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1

5

10

15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20

25

30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35

40

45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50	55	60
Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala		
65	70	75 80
Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile		
	85	90 95
Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe		
	100	105 110
Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu		
	115	120 125
Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala		
	130	135 140
Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu		
145	150	155 160
Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr		
	165	170 175
Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly		
	180	185 190
Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser		
	195	200 205

Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr

210

215

220

Pro Ser Gly Met Val Phe His Arg Val

225

230

<210> 8

<211> 2409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(923)

<400> 8

acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag tttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5

10

15

20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40

45

50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55

60

65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70

75

80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85

90

95

100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572

Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

105

110

115

gac att gcc ttc aag cta aac aac caa atc aga gaa aat gca gaa gtc 620

Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val

120

125

130

19/735

tcc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg 668
 Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp

135 140 145

act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc 716
 Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe

150 155 160

aca tct ccc aag act cca gag cat gag ggc cgt tac tat gaa tgt gat 764
 Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp

165 170 175 180

gtc ctt cct tac gcc cag cat ctt cat cat tat ggt gtg gta ttg gag 812
 Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu

185 190 195

gag gat cac cat gat gtc ccg acc ccc agt gct tct gga aaa agt cat 860
 Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His

200 205 210

ctt tgc cct tgg gat ttc cat gac ctt tat caa tat ccc agt gga atg 908
 Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met

215 220 225

gtt ttc cat cgg gtt tgactggacc tggatgctgc tgtttgggtga catccgacag 963
 Val Phe His Arg Val

230

ggcatcttct atgcgatgct tctgtccttc tggatcatct tctgtggcga gcacatgatg 1023

gatcagcacg agcggaaacca catcgcaggg tattggaagc aagtcggacc cattgccgtt 1083

ggctccttct gcctcttcat atttgacatg tgtgagagag gggtaacaact cacgaatccc 1143

ttctacagta tctggactac agacattgga acagagctgg ccatggcctt catcatcgtg 1203

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atgactgtca tcttcttcat cgtagtcag gtaacggaag gccattggaa atggggcggc 1443

gtcacagtcc aagtgaacag tgcctttttc acaggcatct atgggatgtg gaatctgtat 1503

gtctttgctc tgatgttctt gtatgcacca tccataaaa actatggaga agaccagtcc 1563

aatggcgatc tgggtgtcca tagtggggaa gaactccagc tcaccaccac tatcaccat 1623

gtggacggac cactgagat ctacaagttg acccgcaagg aggcccagga gtaggaggct 1683

gcagcgcccg gctgggacgg tctctccata cccagcccc tctaactaga gtggggagca 1743

tgccagagag agctcaatgt acaaatgaat gcctcatggc tcttagctgt ggtttcttgg 1803

accagcggca tggacatttg tcagtttgcc ttctgacggt agcttttggg ggaagattcc 1863

tgcagccact aatgcattgt gtatgataac aaaaactctg gtatgacaca ttttctgtga 1923

tcattgttaa ttagtgacat agtaacatct gtagcagctg gttagtaaac ctcatgtggg 1983

ggtgggggtgg ggggtgtattc ctggggggat ggtttgggcc gaatggggag tggaatattt 2043

gacatttttc ctgttttaaa ttctaggata gattttaaca tcctttgcgg tcccagtcca 2103

aggtaggctg gtgtcatagt ctctcactc ctaatccatg accactgttt ttttcctatt 2163

tatatcacca ggtagccac tgagttaata ttttaagttgt caatagataa gtgtccctgt 2223

tttgtggcat aatataactg aatttcatga gaagatttat tccaccaggg gtatttcagc 2283

tttgaaacca aatctgtgta tctaatacta accaatctgt tggatgtggg ttttaaaaaa 2343

tgtttgctaa actaccaag taagatttac tgtattaaat ggccttcggg tctgaaaagc 2403

tttttt 2409

<210> 9

<211> 198

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu Ser

1	5	10	15
Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp			
20	25	30	
Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro			
35	40	45	
Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys			
50	55	60	
Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro			
65	70	75	80
Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg			
85	90	95	
Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu			
100	105	110	
Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile			
115	120	125	
Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp			
130	135	140	
Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala			
145	150	155	160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln
165 170 175

Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp
180 185 190

Arg His Val Val Leu Ser
195

<210> 10

<211> 1498

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86).. (679)

<400> 10

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ctgtgggacc gctgggcccc cagcg atg gcg acc ctg tgg gga ggc ctt ctt 112

Met Ala Thr Leu Trp Gly Gly Leu Leu

1

5

cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160

Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu

10

15

20

25

ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208
 Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg

30 35 40

tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256
 Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr

45 50 55

aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304
 Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu

60 65 70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352
 Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys

75 80 85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att 400
 Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile

90 95 100 105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat 448
 Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Tyr Met Val Tyr

110 115 120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496
 Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala

125 130 135

cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca 544
 Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala
 140 145 150

aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg 592
 Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu
 155 160 165

aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag 640
 Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu
 170 175 180 185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa 689
 Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser
 190 195

ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggtttt 749

gctgggttttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaact 809

ggaagcaaaa acttgcttga tttttttttc ttgttaacgt aataatagag acatttttaa 869

aagcacacag ctcaaagtca gccataagt cttttcctat ttgtgacttt tactaataaa 929

aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctctttttc 989

accacatagt ttttaactga ctttcaagat aattttcagg gtttttgttg ttgttgtttt 1049

ttgtttgttt gttttggtgg gagaggggag ggatgcctgg gaagtgggta acaacttttt 1109

tcaagtcact ttactaaaca aacttttgta aatagacctt accttctatt ttcgagtttc 1169

atttatattt tgcagtgtag ccagcctcat caaagagctg acttactcat ttgacttttg 1229

cactgactgt attatctggg tatctgctgt gtctgcactt catggtaaac gggatctaaa 1289

atgcctgggtg gcttttcaca aaaagcagat tttcttcatg tactgtgatg tctgatgcaa 1349

tgcacccctag aacaaactgg ccatttgcta gtttactcta aagactaaac atagtcttgg 1409

tgtgtgtggt cttactcatc ttctagtacc tttaaggaca aatcctaagg acttgacac 1469

ttgcaataaa gaaattttat tttaaaccc 1498

<210> 11

<211> 221

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly

1

5

10

15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu

20

25

30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

27/735

35	40	45
Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro		
50	55	60
Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu		
65	70	75 80
Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu		
85	90	95
Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile		
100	105	110
Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe		
115	120	125
Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala		
130	135	140
Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp		
145	150	155 160
Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly		
165	170	175
Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe		
180	185	190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr
 195 200 205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr
 210 215 220

<210> 12

<211> 1864

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153).. (815)

<400> 12

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cccctcggcc tcccagcgct cccaagccgc agcggccgcg ccccttcagc tagctcgctc 120

gctcgctctg cttccctgct gccggctgcg cc atg gcg ttg gcg ttg gcg gcg 173

Met Ala Leu Ala Leu Ala Ala

1

5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221

Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln

10

15

20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269
 Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro

25 30 35

cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317
 Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr

40 45 50 55

aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365
 Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr

60 65 70

aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413
 Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr

75 80 85

atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat 461
 Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp

90 95 100

ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg 509
 Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met

105 110 115

tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg 557
 Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu

120 125 130 135

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605

Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser

140

145

150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc 653

Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser

155

160

165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701

Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val

170

175

180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749

Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr

185

190

195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797

Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr

200

205

210

215

aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttcctg 845

Arg Val Leu Phe Ile Tyr

220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtgaa tcaagatgca 905

gaacacagag gaataatcac ctgctttaa aaaataaagt actgttgaaa agatcatttc 965

tctctatttg ttcttaggtg taaaatttta atagttaatg cagaattctg taatcattga 1025

atcattagtg gttaatgttt gaaaaagctc ttgcaatcaa gtctgtgatg tattaataat 1085

gccttatata ttgtttgtag tcattttaag tagcatgagc catgtccctg tagtcggtag 1145

ggggcagtct tgctttattc atcctccatc tcaaaatgaa cttggaatta aatattgtaa 1205

gatatgtata atgctggcca ttttaaaggg gttttctcaa aagttaaact tttgctatga 1265

ctgtgttttt gcacataatc catatttgct gttcaagtta atctagaaat ttattcaatt 1325

ctgtatgaac acctggaagc aaaatcatag tgcaaaaata catttaaggt gtggtcaaaa 1385

ataagtcttt aattggtaaa taataagcat taatttttta tagcctgtat tcacaattct 1445

gcggtacctt attgtaccta agggattcta aagggtgtgt cactgtataa aacagaaagc 1505

actaggatac aaatgaagct taattactaa aatgtaattc ttgacactct ttctataatt 1565

agcgttcttc acccccaccc ccacccccac ccccttatt ttcttttgt ctctgggtga 1625

ttaggccaaa gtctgggagt aaggagagga ttaggtactt aggagcaaag aaagaagtag 1685

cttggaaactt ttgagatgat ccctaacata ctgtactact tgcttttaca atgtgttagc 1745

agaaaccagt gggttataat gtagaatgat gtgctttctg cccaagtggg aattcatctt 1805

ggtttgctat gttaaaactg taaatacaac agaacattaa taaatatctc ttgtgtagc 1864

<210> 13

<211> 242

<212> PRT

<213> Homo sapiens

<400> 13

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

1 5 10 15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln

100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115 120 125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
130 135 140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145 150 155 160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225 230 235 240

Leu Leu

<210> 14

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(738)

<400> 14

gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg 51

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

1 5 10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15 20 25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala

30 35 40 45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50 55 60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243

Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291

Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

35/735

80

85

90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339

Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu

95

100

105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387

Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe

110

115

120

125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435

Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu

130

135

140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483

Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser

145

150

155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531

Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly

160

165

170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp

175

180

185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627

Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe

190

195

200

205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675
 Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu

210 215 220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723
 Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

225 230 235

tat ttc ttc tta ttg tagagactgc atcaaccgga cattcctttc ttataccaat 778
 Tyr Phe Phe Leu Leu

240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc ttttaagtatc tatatttcat ttgttttgca catatgcata 958

tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag 1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa 1138

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atgaaacatc ttttgttata taggggtgtat tgaaacctgc agtgctgatt attagaaagg 1258

atttgtcaga tttttgaaca tgatatattac attattattt aggaaaactc ttcctgtaaa 1318

taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattta gaaacgtgag tgttaaagat agaatttggt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

ggacatacta gtttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

tctgtttttc ctttcggtta tatcttttgt tttgaatacc aacatttaaa atgatggtat 2098

tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158

cttattttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218

catttcctaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278

cattgtcttt gataaataaa acagttttgt ttgctaata tagcct 2324

<210> 15

<211> 242

<212> PRT

<213> Homo sapiens

<400> 15

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

1 5 10 15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln
100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
115 120 125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
130 135 140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145 150 155 160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225 230 235 240

Leu Leu

<210> 16

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13).. (738)

<400> 16

gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg 51

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

1

5

10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15

20

25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala

30

35

40

45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50	55	60	
gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat			243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr			
65	70	75	
ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat			291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp			
80	85	90	
gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa			339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu			
95	100	105	
aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc			387
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe			
110	115	120	125
agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg			435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu			
130	135	140	
gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc			483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser			
145	150	155	
ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga			531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly			
160	165	170	

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp

175 180 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe

190 195 200 205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu

210 215 220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

225 230 235

tat ttc ttc tta ttg tagagactgc atcaaccoga cattcctttc ttataccaat 778
Tyr Phe Phe Leu Leu

240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc ttaagtatc tatatttcat ttgttttgca catatgcata 958

tgtgcccatt taagatatct gcatatactt gatagaaacc ataaagttgt agcagtttaag 1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

tcttccagct tgtaaagcc attgacttct gacctgacat ttagtataat aaaaatgaaa 1138

ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac 1198

atgaaacatc ttttgttata taggggtgtat tgaaacctgc agtgctgatt attagaaagg 1258

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actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattta gaaacgtgag tgtaaagat agaatttggt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

ggacatacta gtttaggga ttttcagatg ggaagctgca ttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

tctgtttttc ctttcgggta tatcttttgg tttgaatacc aacatttaaa atgatgggtat 2098

tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158

cctatattatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218

catttcctaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278

cattgtcttt gataaataaa acagttttgt tttgctaata tagcct 2324

<210> 17

<211> 336

<212> PRT

<213> Homo sapiens

<400> 17

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met

1

5

10

15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

20

25

30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

35	40	45
Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro		
50	55	60
Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly		
65	70	75 80
Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp		
85	90	95
His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu		
100	105	110
Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro		
115	120	125
Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr		
130	135	140
Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr		
145	150	155 160
Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro		
165	170	175
Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala		
180	185	190

Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
195 200 205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
210 215 220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225 230 235 240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
245 250 255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
260 265 270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
275 280 285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
290 295 300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
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<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(1060)

<400> 18

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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

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ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

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60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
 Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
 70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
 Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
 85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
 115 120 125 130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490
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 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
 165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634

Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
215 220 225

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Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
230 235 240

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Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
245 250 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
260 265 270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275 280 285 290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu

295

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ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018

Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu

310

315

320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060

Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

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tagagactgc atcaaccga cattccttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

tttaagtatc tatatttcac ttgttttgca catatgcata tgtgcccatt taagatattt 1300

gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaagcc 1420

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<212> PRT

<213> Homo sapiens

<400> 19

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Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

20 25 30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

35 40 45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro

50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly

65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp

53/735

	85	90	95
His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu			
	100	105	110
Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro			
	115	120	125
Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr			
	130	135	140
Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr			
145	150	155	160
Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro			
	165	170	175
Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala			
	180	185	190
Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile			
	195	200	205
Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln			
	210	215	220
Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala			
225	230	235	240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
245 250 255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
260 265 270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
275 280 285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
290 295 300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
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Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

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agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298

Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

70

75

80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346

Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85

90

95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394

Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn	
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tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg	442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro	
115	120 125 130
cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct	490
Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser	
	135 140 145
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Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser	
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Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser	
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gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct	634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala	
	180 185 190
gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag	682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu	
	195 200 205 210
gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga	730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg	



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Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile			
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Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile			
245	250	255	
gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874			
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys			
260	265	270	
tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922			
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn			
275	280	285	290
gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970			
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu			
295	300	305	
ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018			
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu			
310	315	320	
agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060			
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu			
325	330	335	

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<213> Homo sapiens

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Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn

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Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

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<210> 22

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<212> DNA

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cggcctccgc ggtgcctgcc ttgcctctca ggttgaggag ctcaagcttg ggaaa atg 178

Met

1

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Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys

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10

15

aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274

Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser

20

25

30

cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322

Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys

35

40

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ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370

Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys

50

55

60

65

gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttctaaagg 423

Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

70

75

accccatcat ttaaaaaatg gacctgataa tatgaagcat cttccttgta attgtctctg 483

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tt 1085

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<211> 84

<212> PRT

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20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp

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Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser

65 70 75 80

Leu Ser Gly Leu

<210> 24

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65)..(316)

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cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile

1

5

10

15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157

Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys

20

25

30

gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205

Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln

35

40

45

att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253

Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr

50

55

60

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301

Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His

65

70

75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356

Ser Leu Ser Gly Leu

80

gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggcttttagac 416

attggtggga ccaaggatgt tttgcaggat gccctgatcc taagaagggg gcctgggggt 476

gcgtgcagcc tgtcggggag accccactct gtgcacctat tggctcttct agctgactct 536

tctcgttggg cttagagtct gcctgtttct gctagctccg tgtttagtcc acttgggtca 596

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<212> PRT

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Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala

50

55

60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys

65

70

75

80

Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln

85

90

95

Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met

100

105

110

Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly

115

120

125

Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile

130

135

140

Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr

145

150

155

160

Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala

165

170

175

Leu Leu Phe

<210> 26

<211> 1820

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114)..(650)

<400> 26

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acgcggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg 116

Met

1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164

Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro

5

10

15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212

Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu

20

25

30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260

Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro

35

40

45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308

Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val

50

55

60

65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg 356
 Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr

70 75 80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg 404
 Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu

85 90 95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc 452
 Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val

100 105 110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg 500
 His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu

115 120 125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg 548
 Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly

130 135 140 145

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt 596
 Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe

150 155 160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg 644
 Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu

165 170 175

ctc ttc tgagcccgtc tcccggacag gttgaggaag ctgctccaga agcgcctcgg 700

Leu Phe

aaggggagct ctcatcatgg cgcgtgctgc tgcggcatat ggacttttaa taatgttttt 760

gaatttcgta ttctttcatt ccactgtgta aagtgctaga cattttccaa tttaaaattt 820

tgctttttat cctggcactg gcaaaaagaa ctgtgaaagt gaatttattc agccgactgc 880

cagagaagtg ggaatggtat aggattgtcc ccaagtgtcc atgtaacttt tgttttaacc 940

tttgacactt ctcagtgtg tatgcggtg cagccgtctc acctgtttcc ccacaaaggg 1000

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aaggtgaata agtgacaaat aaagccagtt tttacaagg 1820

<210> 27

<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1 5 10 15

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

20 25 30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35 40 45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

50	55	60
Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe		
65	70	75 80
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val		
	85	90 95
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp		
100	105	110
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe		
115	120	125
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His		
130	135	140
His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro		
145	150	155 160
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val		
	165	170 175
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln		
180	185	190
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln		
195	200	205

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
210 215 220

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225 230 235 240

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
245 250 255

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
260 265 270

Ile Ala Lys Val Lys Ala Asn
275

<210> 28

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(955)

<400> 28

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tgctccctcc gagcgctccg ccgttgcccg cctggcccct acggagtcct tagccagg 118

atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1 5 10 15

ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214
Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

20 25 30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262
Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35 40 45

atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc 310
Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

50 55 60

tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc 358
Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe

65 70 75 80

ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg 406
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val

85 90 95

gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg 454
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp

100 105 110

ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt 502
 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe

115

120

125

att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat 550
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His

130

135

140

cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg 598
 His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro

145

150

155

160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc 646
 Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val

165

170

175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa 694
 Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180

185

190

ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag 742
 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195

200

205

ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc 790
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser

210

215

220

tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc 838

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
 225 230 235 240

acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc 886
 Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
 245 250 255

aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt 934
 Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
 260 265 270

att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgcccacc 985
 Ile Ala Lys Val Lys Ala Asn
 275

taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct 1045

gtgaccaagg cttatgtggt caggactgag caggggactg gccctcccct cccacagct 1105

gctctacagg gaccacggct ttggttcctc acccacttcc cccgggcagc tccagggatg 1165

tggcctcatt gctgtctgcc actccagagc tgggggctaa aagggtgta cagttatttc 1225

cccctccctg ccttaaaact tgggagagga gcactcaggg ctggccccac aaagggtctc 1285

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tcctccaccc cacacactga agcagtagct tctgggccaa aggtcagggt gggcgggggc 1405

ctgggaatac agcctgtgga ggctgcttac tcaacttggtg tcttaattaa aagtgcaga 1465

ggaaacc

1472

<210> 29

<211> 137

<212> PRT

<213> Homo sapiens

<400> 29

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1 5 10 15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35 40 45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50 55 60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65 70 75 80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

85 90 95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
100 105 110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala
115 120 125

Tyr Met Asp Ala Pro Lys Ala Ala Leu
130 135

<210> 30

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145).. (555)

<400> 30

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ggaaattgaa actgagtggc ccacgatggg aagaggggaa agcccagggg tacaggaggc 120

ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171

Met Gly Phe Gly Ala Thr Leu Ala Val

1

5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc 219

79/735

Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe
 10 15 20 25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267
 Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro
 30 35 40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315
 Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro
 45 50 55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363
 Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly
 60 65 70

tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca 411
 Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro
 75 80 85

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc 459
 Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala
 90 95 100 105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc 507
 Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser
 110 115 120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555
 Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu
 80/735

tgagcattcc ctggcctctc tggctgccac ttggttatgt tgtgtgtgtg cgtgagtgg 615

gtgcaggcgc gggttccttac gcccctatgtg tgctgtgtgt gtccaggcac gggttccttac 675

gcccctatgtg tgctgtgtgt gtcctgcctg tatatgtggc ttcctctgat gctgacaagg 735

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accctagggt gaccaagtag ggctgtcac accagggtgg cgcagcttctc tgtgtgatgc 975

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caagttggac tttgatcctt tgggcagatg tccattgct ccctggagcc tgtcatgcct 1155

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 attactgttt caccagagct gtcttagctc aaatctgttg tgtttctgag tctagggtct 1755
 gtacacttgt ttataataaa tgcaatcggt tgg 1788

<210> 31

<211> 118

<212> PRT

<213> Homo sapiens

<400> 31

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1 5 10 15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35

40

45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50

55

60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65

70

75

80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

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95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

100

105

110

Glu Cys Pro Cys Gln Leu

115

<210> 32

<211> 1908

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (444)

<400> 32

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83/735

ggaggcctct gggatgaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc 114

Met Gly Phe Gly Ala Thr Leu Ala

1

5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162

Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys

10

15

20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210

Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg

25

30

35

40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258

Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr

45

50

55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306

Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln

60

65

70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354

Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr

75

80

85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402

Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro

90

95

100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444

Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu

105

110

115

tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac 504

atcactcaac aggcctctgc ccctttctgc ttgcctgcca ctcacacggc agcccacccat 564

gtcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624

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 tttataataa atgcaatcgt ttgg 1908

<210> 33

<211> 168

<212> PRT

<213> Homo sapiens

<400> 33

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln

1 5 10 15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala

20 25 30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro

35 40 45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala

50 55 60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val

65 70 75 80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro

85 90 95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala

100 105 110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro

115 120 125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly

130 135 140

Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly
145 150 155 160

Ser Asp Gly Gly Tyr Thr Ile Trp
165

<210> 34

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (573)

<400> 34

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gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro

1

5

10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159

Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro

15

20

25

30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207

Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr

35

40

45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255

Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser

50

55

60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303

Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val

65

70

75

gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc 351

Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val

80

85

90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat 399

Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr

95

100

105

110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447

Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro

115

120

125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495

Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met

130

135

140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543

Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met

89/735

145

150

155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc 593

Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp

160

165

tgtgccggga aagacatcac ataccttcag cacttctcac aatgtaactg ctttagtcat 653

attaacctga agttgcagtt tagacacatg ttgttggggt gtctttcttg tgcccaaact 713

ttcaggcact tttcaaattt aataaggaac catgtaatgg tagcagtacc tccctaaagc 773

at ttgtgaggt aggggaggta tccattcata aaatgaatgt ggggtgaagcc gccctaagga 833

ttttccttta atttctctgg agtaatactg taccatactg gtctttgctt ttagtaataa 893

aacatcaaat taggtttgga gggaactttg atcttcctaa gaattaaagt tgccaaatta 953

ttctgattgg tctttaatct cctttaagtc ttgatatat attacttggt ataaatggaa 1013

cgcattagtt gtctgccttt tcctttccat cccttgcccc acccatccca tctccaaccc 1073

tagtcttcca tttcctcccg ccagtctcca ttgaatcaat ggtgcaggac agaaagccag 1133

tcagactaat ttctttcttt cctcgcaatt ctccccactc gtcacttttt aactagtgtt 1193

tcacaaggat cctctgaaac cctctctgtg cccaagtac agatgccatt acttctgctt 1253

tcgtatctcc tcaggcaaaa gtggagggtg ccttatgggc cctcctcata ggttgtctct 1313

gcatacacga acctaacca aatttgcttt ggtgccagaa aaactgagct atgtttgaac 1373

aaagatgtcg tgcaaactgt actgtgaaca acagttgggt taaaatatga ggggcaagga 1433

ggaggatgca tttcaaaagc ttgattgatg tggtcagagc taaattaaga ggagttttca 1493

gatcaaaaac tggttaccat tttttgtcag agtgtctgat gcggccactc attcggtcc 1553

ccagaattcc tagactgggt taatagggtc atattgtgaa tgtctcacta caaatgact 1613

tgagtccagt gaaatctcat tagggtttaa gaatatttca gggatcctta atgttttgat 1673

ttttgttttc tgaaattgga ttttatttta ttttatctta taatttcagt tcatctaaat 1733

tgtgtgttct gtacatgtga tgtttgactg taccattgac tgttatggaa gttcagcggt 1793

gtatgtctct ctctacactg tgggtgcactt aacttgtgga atttttatac taaaaatgta 1853

gaataaagac tattttgaag atttgaataa agtgatgaag ttgc 1897

<210> 35

<211> 455

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu

1	5	10	15
Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp			
20	25	30	
Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe			
35	40	45	
Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly			
50	55	60	
Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys			
65	70	75	80
Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr			
85	90	95	
Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe			
100	105	110	
Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly			
115	120	125	
Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu			
130	135	140	
Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu			
145	150	155	160

Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
165 170 175

Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg
180 185 190

Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala
195 200 205

Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
210 215 220

Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
225 230 235 240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu
245 250 255

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
260 265 270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
275 280 285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
290 295 300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr
305 310 315 320

Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val

325

330

335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile

340

345

350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr

355

360

365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala

370

375

380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met

385

390

395

400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu

405

410

415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val

420

425

430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala

435

440

445

Pro Glu Lys Gln Met Ala Pro

450

455

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1480)

<400> 36

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tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118

Met

1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166

Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe

5

10

15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214

Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr

20

25

30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262

Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala

35

40

45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310

Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val
50 55 60 65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358
Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val
70 75 80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt 406
Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe
85 90 95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc 454
Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser
100 105 110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat 502
Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp
115 120 125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag 550
Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln
130 135 140 145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt 598
Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu
150 155 160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc 646
Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe

165	170	175	
ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg	694		
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu			
180	185	190	
ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg	742		
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met			
195	200	205	
gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca	790		
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser			
210	215	220	225
ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt	838		
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser			
230	235	240	
gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta	886		
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu			
245	250	255	
agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag	934		
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu			
260	265	270	
aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt	982		
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu			
275	280	285	

ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc 1030
 Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr
 290 295 300 305

atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga 1078
 Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg
 310 315 320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag 1126
 Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys
 325 330 335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc 1174
 Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val
 340 345 350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc 1222
 Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala
 355 360 365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag 1270
 Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln
 370 375 380 385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt 1318
 Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser
 390 395 400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg 1366
Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu
405 410 415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414
Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser
420 425 430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462
Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro
435 440 445

gag aag caa atg gca cct tgaacttaag cctactacag actgttagag 1510
Glu Lys Gln Met Ala Pro
450 455

gccagtgggtt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570

ttataaaca acaaaatgct atggtagcat ttttcacctt catagcatac tccttccccg 1630

tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagaggag aactaactca 1690

agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggcggagagg 1750

agccaagaaa ctaaagggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810

gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaaaaggt tatagctttg 1870

ccttgagatt gactcattaa aatcagagac tgt 1903

<210> 37

<211> 322

<212> PRT

<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser
1 5 10 15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala
20 25 30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser
35 40 45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile
50 55 60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser
65 70 75 80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met
85 90 95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala
100 105 110

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp
115 120 125

Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu
130 135 140

Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu
145 150 155 160

Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val
165 170 175

Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp
180 185 190

Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe
195 200 205

Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr
210 215 220

Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu
225 230 235 240

Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly
245 250 255

Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg
260 265 270

Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His

275

280

285

Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser

290

295

300

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp

305

310

315

320

Phe Gln

<210> 38

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292)..(1257)

<400> 38

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ccctgccccg cccctcccc tcggcctcgc ggcgacggcg gcggtggcgg cttggacgac 120

tcggagagcc gaggtaagac atttcacct ggacacctga ccatgtgcct gccctgagca 180

gcgaggccca ccaggcatct ctgttgtggg cagcagggcc aggtcctggt ctgtggaccc 240

tcggcagttg gcaggctccc tctgcagtgg ggtctggggc tcggccccac c atg tcg 297

Met Ser

1

agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc 345

Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser

5

10

15

acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca 393

Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala

20

25

30

gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca 441

Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala

35

40

45

50

gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt 489

Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser

55

60

65

gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac 537

Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr

70

75

80

tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc 585

Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly

103/735

85

90

95

gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg 633

Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala Ser Leu

100

105

110

ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc 681

Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser

115

120

125

130

aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc 729

Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser

135

140

145

aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg 777

Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu

150

155

160

cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag 825

Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu

165

170

175

cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag 873

His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu

180

185

190

gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac 921

Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr

195

200

205

210

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca	969
Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala	
215 220 225	
ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag	1017
Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu	
230 235 240	
tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag	1065
Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys	
245 250 255	
aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac	1113
Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn	
260 265 270	
tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att	1161
Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile	
275 280 285 290	
tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct	1209
Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala	
295 300 305	
ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag	1257
Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln	
310 315 320	

tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcaactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377

tcacagattt cattcctgtt tttatatata tattttttgt tgtcgtttta acatctccac 1437

gtccctagca t 1448

<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn

1 5 10 15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His

20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu

35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys

50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu

65 70 75 80

Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu
85 90 95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe
100 105 110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly
115 120 125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile
130 135 140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val
145 150 155 160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala
165 170 175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly
180 185 190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val
195 200 205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr
210 215 220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met
107/735

225 230 235 240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser

245 250 255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu

260 265 270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro

275 280 285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys

290 295 300

Gln Met His Ile Trp Met Ser Ser Thr

305 310

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153).. (1091)

<400> 40

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108/735

ctccagccgc ccgcgggcca gcgcaccggt cccccagcgg cagccgagcc cgccccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173

Met Ala Gly Gln Pro Gly His

1

5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221

Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro

10

15

20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269

Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg

25

30

35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317

Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln

40

45

50

55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg 365

Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val

60

65

70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413

Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg

75

80

85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461

Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro

109/735

90	95	100	
aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac			509
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn			
105	110	115	
att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag			557
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys			
120	125	130	135
tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag			605
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys			
	140	145	150
tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg			653
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg			
	155	160	165
gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg			701
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr			
	170	175	180
ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct			749
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser			
185	190	195	
gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca			797
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser			
200	205	210	215

ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg	845
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp	
220 225 230	
tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc	893
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe	
235 240 245	
tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag	941
Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln	
250 255 260	
tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga	989
Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg	
265 270 275	
gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac	1037
Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp	
280 285 290 295	
atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc	1085
Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser	
300 305 310	
agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgccttac	1141
Ser Thr	
ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt	1201

tcagcaggtt ccccaaaagg ctgcccagcc ttacagcaga tgctgaaggc agagcagctg 1261
 agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321
 gttgtggaca atctcagctg ggtcaataag ggcaggtggt tcagcgagcc acggcagccc 1381
 cctgtatctg gattgtaatg tgaatcttta gggtaattcc tccagtgacc tgtcaaggct 1441
 tatgctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgagcct ttgaaaatgg 1501
 ttagtaccgg gttcagttta gttcttggtta tcttttcaat caagctgtgt gcttaattta 1561
 ctctgttgta aagggataaa gtggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro

1 5 10 15

Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr

20 25 30

Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln

35

40

45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr

50

55

60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro

65

70

75

80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln

85

90

95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn

100

105

110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro

115

120

125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn

130

135

140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala

145

150

155

160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr

165

170

175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe

180

185

190

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
195 200 205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
210 215 220

Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
225 230 235 240

Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
245 250 255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
260 265 270

Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
275 280 285

Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
290 295 300

Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305 310 315 320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
325 330 335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
340 345 350

Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg

355

360

365

Ala Lys Glu

370

<210> 42

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(1203)

<400> 42

attggccatc accgcgcggc cgcgcagcgg acaccgtgcg taccggcctg cggcgcccgg 60

ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114

Met Ser His Glu Lys Ser Phe Leu

1

5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162

Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly

10

15

20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc 210

115/735

Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala
 25 30 35 40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258
 Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly
 45 50 55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt 306
 Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly
 60 65 70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc 354
 Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly
 75 80 85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat 402
 Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr
 90 95 100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc 450
 Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe
 105 110 115 120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag 498
 Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu
 125 130 135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg 546
 Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp
 116/735

140	145	150	
gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg			594
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val			
155	160	165	
ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act			642
Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr			
170	175	180	
ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac			690
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr			
185	190	195	200
tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt			738
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys			
205	210	215	
tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg			786
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser			
220	225	230	
gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc			834
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe			
235	240	245	
tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc			882
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val			
250	255	260	

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc 930
 Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
 265 270 275 280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc 978
 Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe
 285 290 295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac 1026
 Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
 300 305 310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc 1074
 Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
 315 320 325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat 1122
 Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
 330 335 340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170
 Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
 345 350 355 360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
 Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
 365 370

gtgcccgctc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283
 tacttcccct ctctcttgtc ccagggcaca gcctagggaa aaggatgcct ctctccaacc 1343
 ctctgtatg tacactgcag atacttccat ttggaccgcg tgtggccaca gcatggcccc 1403
 tttagtcctc ccgccccgcg caaggggcag caaggccacg tttcgtgcc acctcctgtc 1463
 tactcattgt tgcattgagc ctgtctgcc gccacccca gggactgggg gcagcaccag 1523
 gtcccgggga gagggattga gccaagaggt gagggtgac gtcttcctc ctgtcccagc 1583
 tccccagcct ggcgtagagc accctcccc tccccccac cccctggag tgctgccctc 1643
 tggggacatg cggagtgggg gtcttatccc tgtgtgagc cctgagggca gagaggatgg 1703
 catgtttcag gggaggggga agccttcctc tcaatttggt gtcagtgaat ttccaataaa 1763
 tgggatttgc tctctgcc 1781

<210> 43

<211> 393

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

1

5

10

15

119/735

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20

25

30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35

40

45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50

55

60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65

70

75

80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85

90

95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100

105

110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg

115

120

125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln

130

135

140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala

145

150

155

160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala

120/735

	165	170	175
Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val			
	180	185	190
Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu			
	195	200	205
Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser			
	210	215	220
Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr			
	225	230	235
			240
His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly			
	245	250	255
Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly			
	260	265	270
Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala			
	275	280	285
Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr			
	290	295	300
Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn			
	305	310	315
			320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu

325

330

335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

340

345

350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

355

360

365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370

375

380

Leu Val Pro Gly Pro Glu Lys Glu Asn

385

390

<210> 44

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50).. (1228)

<400> 44

agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac 58

Met Ser Asp

1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg	106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro	
5 10 15	
cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc	154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser	
20 25 30 35	
gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta	202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu	
40 45 50	
gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg	250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg	
55 60 65	
ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg	298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu	
70 75 80	
cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg	346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu	
85 90 95	
tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg	394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala	
100 105 110 115	

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
 Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
 120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
 Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
 135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
 Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
 150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
 Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
 165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634
 Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
 180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
 Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
 200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
 Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
 215 220 225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778
 124/735

Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr

230

235

240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826

Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile

245

250

255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874

Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu

260

265

270

275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922

Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu

280

285

290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970

Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn

295

300

305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018

Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val

310

315

320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066

Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser

325

330

335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114

Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys

125/735

340

345

350

355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162

Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met

360

365

370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210

Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro

375

380

385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac 1258

Gly Pro Glu Lys Glu Asn

390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct cctcccccg aagttctctg tggatgatgac cgctctcccc 1378

tgccccctcc cgcttccctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438

ccctgccaaag gcgacaggga gggtcagagg gaggccggct gcttcctgcc cccacccttt 1498

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ccctagtgtc ccttcagcct gggctgacca gtgcccgcct ctgggcttga ccagttccca 1738

atctcgtcct ctgtcccaa ctcttaagc acaattgggc ttcttccatc tccaggtttt 1798

ctgccattct taaccaaggc agccccaagc ctcttggga ggcaggga aaacaggtgc 1858

cctcatcgtg gtctgtgcca tgtccgtct ctatggtggt tgaggagaaa ggcggggaag 1918

cttcctcagc ctgagata tgtgtggcat ttactagcca gagctctgaa aggcagtgc 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttagg 2038

gaggccctac tgccttctca aagcagagag gcagcttata aaactcagcc caaaactctg 2098

tttcatggg tggggagatg gagcaggga gtacagagt ggatggtcag gacctgggcc 2158

attgcaacca aaatggggac ttcttggta gggaggtcac tccctctact cactgagcta 2218

ggattaggga gggttattgc cccaaccatt gcaatgggag gtggaggga aggctcagcc 2278

tcctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

accaccccat taccacagct gcctttgtgt gttgtgtca ataaaaagcc aaaccctg 2396

<210> 45

<211> 393

<212> PRT

<213> Homo sapiens

<400> 45

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

1 5 10 15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20 25 30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg

115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln

130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala

128/735

145	150	155	160
Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala			
165	170	175	
Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val			
180	185	190	
Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu			
195	200	205	
Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser			
210	215	220	
Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr			
225	230	235	240
His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly			
245	250	255	
Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly			
260	265	270	
Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala			
275	280	285	
Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr			
290	295	300	

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
305 310 315 320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
325 330 335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
340 345 350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
355 360 365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
370 375 380

Leu Val Pro Gly Pro Glu Lys Gln Asn
385 390

<210> 46

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50).. (1228)

<400> 46

agctgtgcac tctccatcca gctgtgcgct ctgctcgga gtcccagcc atg tcc gac 58

Met Ser Asp

1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106

Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

30

35

gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta 202

Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250

Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70

75

80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346

Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85

90

95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394

131/735

Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
 100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
 Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
 120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
 Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
 135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
 Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
 150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
 Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
 165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634
 Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
 180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
 Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
 200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
 Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
 132/735

215	220	225	
gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act			778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr			
230	235	240	
gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att			826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile			
245	250	255	
gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc			874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu			
260	265	270	275
ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg			922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu			
280	285	290	
acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat			970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn			
295	300	305	
cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg			1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val			
310	315	320	
tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt			1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser			
325	330	335	

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
 Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
 340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
 Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
 360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
 Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
 375 380 385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac 1258
 Gly Pro Glu Lys Gln Asn
 390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

.ctgtcataat gctctgccct ccctcccccg aagttctctg tggatgatgac cgctctcccc 1378

tgccccctccc cgcttctctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438

ccctgccaag gcgacaggga gggtcagagg gaggccggct gcttcctgcc cccacccttt 1498

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atctcgtcct ctgtccccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798

ctgccattct taaccaaggc agccccaagc ctcttgggga ggcagggcaa aaacaggtgc 1858

cctcatcgtg gtctgtgcca tgtcccgtct ctatgggtgt tgaggagaaa ggcggggaag 1918

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tttacctggg tggggagatg gagcaggga gtacagagtg ggatgggtcag gacctgggcc 2158

attgcaacca aaatggggac ttcctgggta gggagggtcac tccctctact cactgagcta 2218

ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278

tcctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

accaccccat taccacagt gcctttgtgt gtttgtgtca ataaaaagcc aaacctg 2396

<210> 47

<211> 138

<212> PRT

<213> Homo sapiens

<400> 47

Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly
1 5 10 15

Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys
20 25 30

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
35 40 45

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys
50 55 60

Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile
65 70 75 80

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
85 90 95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val
100 105 110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
115 120 125

Asp Lys Val Gly Glu Ser Asn Asn Met Val
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130

135

<210> 48

<211> 2976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110)..(523)

<400> 48

agacgtggcg gctctcgccct gggctgtttc ccggcttcat ttctcccgac tcagcttccc 60

accctgggct ttccgaggtg ctgtcgccgc tgtccccacc actgcagcc atg atc tcc 118

Met Ile Ser

1

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg 166

Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val

5

10

15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg 214

Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu

20

25

30

35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt 262

Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly

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40	45	50	
tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct			310
Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala			
55	60	65	
aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct			358
Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro			
70	75	80	
ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg			406
Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg			
85	90	95	
ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt			454
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu			
100	105	110	115
gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt			502
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val			
120	125	130	
gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta			553
Gly Glu Ser Asn Asn Met Val			
135			
aaatattgtg ttattttataa agtcatttga agaattattca gcacaaaatt aaattacatg			613
aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag			673
138/735			

caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733

caagcaaact gagagaggig aaatccatgt taatgatgct taagaaactc ttgaaggcta 793

tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc ttagagaact gtggtgcctg 853

tttcttttct ttttattttg aaggctcagg agcatccata ggcatttgct ttttagaaat 913

gtccactgca atggcaaaaa tatttccagt tgcactgtat ctctggaagt gatgcatgaa 973

ttcgattgga ttgtgtcatt ttaaagtatt aaaaccaagg aaacccaat tttgatgtat 1033

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atatttcaaa gccaggtgaa aatctgaact agatattctt tgttggaata tgcaaaggtc 1153

attctttact aacttttagt tactaaatta tagctaagtt ttgtcagcag catactccgg 1213

aaagtctcat acttcttggg agtctgcct cctaagtatc tgtctatata attcattacg 1273

tgtaagtatt taacaaaaaa gcattcttga ccatgaatga agtagtttgt ttcatagctt 1333

gtctcattga atagtattat tgaagatact aaatgatgca aaccaaattg attttttcca 1393

tgtcatgatg taatttttct ttcttctttc ttttttttaa attttagcag tggcttatta 1453

tttgtttttc ataaattaaa ataacttttg ataatgttta cttaagaca tgtaacatgt 1513

taaaagggtta aacttatggc tgtttttaaa gggctattca tttaatctga gttttccctt 1573

attttcagct ttttcctagc atataatagt cattaagcat gacatatcct tcatatgac 1633

actcatcttg agttaattag aaaataacctg agttcacgtg ctaaagtcac ttcactgtaa 1693

taaactgact atggtttctt aagaacatga cactaaaaaa aaagtgggtt tttccaccg 1753

ttgctgatta ttagacagta ggaaatagct gttttcttta gttttacaag atgtgacagc 1813

tttagtggtta gatgtaggga aacatttcaa cagccatagt actatttggt ttaccactga 1873

ttgcactgtt ttgttttttt aacagttgca aagcttttta atgcataaaa gtataattga 1933

aatctgtggt atttatttac aaacatgtct acaaaaatag attacagctt attttatttt 1993

tagttaaatc tcttaataca cagagaactc ccaatcttgc tcatctaaat aaggaaagac 2053

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gttaatggaa taataagagg ctactgttgt gtctaattgt cttcaaaaaa gtaatatcct 2233

cacttggaga gtgtcaaata catactttga ggattgactt tatataaggt gccctgtaga 2293

actctgttac acatattttt gacccatatt atttacaatg tcttgataat tctacctttt 2353

tagagcaaga atagtatctg ctaatgtaag ggacatctgt atttaactcc tttgtagaca 2413

tgaatttcta tcaaaatggt ctttgactg taacagagat tccttttttc aataatctta 2473
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 cagccttctg tctgtaacaa aaatgtactt tatagagatg gaggaaaagg tctaatacta 2773
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 gaatgttttt cttttccct tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893
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 caataaaagg gtacttttct att 2976

<210> 49

<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe

1	5	10	15
His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln			
20	25	30	
Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val			
35	40	45	
Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro			
50	55	60	
Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met			
65	70	75	80
Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile			
85	90	95	
Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser			
100	105	110	
Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu			
115	120	125	
His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp			
130	135	140	
Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg			
145	150	155	160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
165 170 175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
180 185 190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu
195 200 205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
210 215 220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
225 230 235 240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser
245 250 255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
260 265 270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
275 280 285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
290 295 300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
305 310 315 320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser

325

330

335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser

340

345

350

Arg Ser Thr Thr His Leu Ile

355

<210> 50

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (327).. (1403)

<400> 50

cttcaaagca gtcagcaagg tggcaagttg caaaagagct ttatcaaact gaaagtaatt 60

atgttaatat attggcaaca attattcagt tatttcaagt accattggaa gaggaaggac 120

aacgtggtgg acctatcctt gcaccagagg agattaagac tatttttggt agcatcccag 180

atatctttga tgtacacact aagataaagg atgatcttga agaccttata gtttaattggg 240

atgagagcaa aagcattggt gacatttttc tgaaatattc aaaagatttg gtaaaaacct 300

accctccctt tgtaaacttc tttgaa atg agc aag gaa aca att att aaa tgt 353

Met Ser Lys Glu Thr Ile Ile Lys Cys

1

5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401

Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala

10

15

20

25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449

Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro

30

35

40

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497

Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys

45

50

55

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545

His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile

60

65

70

gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa 593

Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys

75

80

85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641

Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly

90

95

100

105

tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt 689
 Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val

110 115 120

gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta 737
 Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val

125 130 135

act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac 785
 Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His

140 145 150

aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca 833
 Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro

155 160 165

gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag 881
 Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys

170 175 180 185

gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg 929
 Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu

190 195 200

ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag 977
 Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln

205 210 215

atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt 1025
Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys
220 225 230

cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att 1073
Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile
235 240 245

tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac 1121
Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp
250 255 260 265

agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag 1169
Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys
270 275 280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga 1217
Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg
285 290 295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc 1265
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser
300 305 310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta 1313
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu
315 320 325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa 1361
147/735

Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu
 330 335 340 345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata 1403
 Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
 350 355

tgaagcgtaa ccaaaatctt aaattataga aatgtataga cacctcatac tcaaataaga 1463

aactgactta aatggtactt gtaattagca cttggtgaaa gctggaagga agataaataa 1523

cactaaacta tgctatttga tttttcttct tgaaagagta aggtttacct gttacatttt 1583

caagttaatt catgtaaaaa atgatatgta ttttgatgta atttatctct tgtttgaatc 1643

tgatcattcaa aggccaataa ttttaagttgc tatcagctga tattagtagc tttgcaacc 1703

tgatagagta aataaatttt atgggcgggt gccaaatact gctgtgaatc tatttgtata 1763

gtatccatga atgaatttat ggaaatagat atttgtgcag ctcaatttat gcagagatta 1823

aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883

ttcacatgtg cagtttgaag tatttaaata accactcctt tcacagttta ttttcttctc 1943

aagcgttttc aagatctagc atgtggattt taaaagattt gccctcatta acaagaataa 2003

catttaaagg agattgtttc aaaatatattt tgcaaattga gataaggaca gaaagattga 2063

gaaacattgt atattttgca aaaacaagat gttttagct gtttcagaga gactacggta 2123
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 gttcaacttt ttattgtggt ctataatta aatgtaaaat tgaaaattca ttgctgttt 2363
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 agtaagaact ttgtaaataa atacctaaaa ccc 2636

<210> 51

<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu

1

5

10

15

149/735

Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
20 25 30

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
35 40 45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
50 55 60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65 70 75 80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val
85 90 95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys
100 105 110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
115 120 125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
130 135 140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
145 150 155 160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg
150/735

	165	170	175
Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln			
	180	185	190
Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys			
	195	200	205
Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe			
	210	215	220
Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe			
225	230	235	240
Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr			
	245	250	255
Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu			
	260	265	270
Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys			
	275	280	285
Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu			
	290	295	300
Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met			
305	310	315	320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
325 330 335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu
340 345 350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe
355 360 365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser
370 375 380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp
385 390 395 400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro
405 410 415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
420 425 430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
435 440 445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
450 455 460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
465 470 475 480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp
485 490 495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu
500 505 510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu
515 520 525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu
530 535 540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu
545 550 555 560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu
565 570 575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr
580 585 590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn
595 600 605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val
610 615 620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser
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625 630 635 640

Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp

645 650 655

Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile

660 665 670

Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly

675 680 685

Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu

690 695 700

Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His

705 710 715 720

Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val

725 730 735

Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp

740 745 750

Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp

755 760 765

Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn

770 775 780

Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys
785 790 795 800

Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro
805 810 815

Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu
820 825 830

Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser
835 840 845

Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu
850 855 860

Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr
865 870 875 880

His Leu Ile

<210> 52

<211> 3910

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (29).. (2677)

<400> 52

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Met Ala Glu Asn Ser Val Leu Thr																
1 5																
tcc	act	act	ggg	agg	act	agc	ttg	gca	gac	tct	tcc	att	ttt	gat	tct	100
Ser	Thr	Thr	Gly	Arg	Thr	Ser	Leu	Ala	Asp	Ser	Ser	Ile	Phe	Asp	Ser	
10			15			20										
aaa	gtt	act	gag	att	tcc	aag	gaa	aac	tta	ctt	att	gga	tct	act	tca	148
Lys	Val	Thr	Glu	Ile	Ser	Lys	Glu	Asn	Leu	Leu	Ile	Gly	Ser	Thr	Ser	
25		30				35				40						
tat	gta	gaa	gaa	gag	atg	cct	cag	att	gaa	aca	aga	gtg	ata	ttg	gtt	196
Tyr	Val	Glu	Glu	Glu	Met	Pro	Gln	Ile	Glu	Thr	Arg	Val	Ile	Leu	Val	
45				50				55								
caa	gaa	gct	gga	aaa	caa	gaa	gaa	ctt	aca	aaa	gcc	tta	aag	gac	att	244
Gln	Glu	Ala	Gly	Lys	Gln	Glu	Glu	Leu	Thr	Lys	Ala	Leu	Lys	Asp	Ile	
60				65				70								
aaa	gtg	ggc	ttt	gta	aag	atg	gag	tca	gtg	gaa	gaa	ttt	gaa	ggc	ttg	292
Lys	Val	Gly	Phe	Val	Lys	Met	Glu	Ser	Val	Glu	Glu	Phe	Glu	Gly	Leu	
75			80			85										
gat	tct	ccg	gaa	ttt	gaa	aat	gta	ttt	gta	gtc	acg	gac	ttt	cag	gat	340
Asp	Ser	Pro	Glu	Phe	Glu	Asn	Val	Phe	Val	Val	Thr	Asp	Phe	Gln	Asp	

90	95	100	
tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca	388		
Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro			
105	110	115	120
cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca	436		
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser			
125	130	135	
tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt	484		
Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe			
140	145	150	
act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc	532		
Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val			
155	160	165	
cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca	580		
His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr			
170	175	180	
cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg	628		
His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val			
185	190	195	200
agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg	676		
Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp			
205	210	215	

gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga 724

Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg

220

225

230

aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg 772

Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu

235

240

245

gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg 820

Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met

250

255

260

caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt 868

Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu

265

270

275

280

gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag 916

Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys

285

290

295

aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg 964

Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met

300

305

310

gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act 1012

Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr

315

320

325

cct gag ctg aag aaa tca gtg tca atg ctt tct cta aat acc cct aac 1060
Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn
330 335 340

agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca 1108
Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser
345 350 355 360

aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct 1156
Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala
365 370 375

gag cat tcc ctt tcc ata ggg tca ctg cta gat atc tcc aac aca cca 1204
Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro
380 385 390

gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct 1252
Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser
395 400 405

tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa 1300
Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln
410 415 420

gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg 1348
Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu
425 430 435 440

gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa 1396

Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln

445

450

455

cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt 1444

Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly

460

465

470

agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt 1492

Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu

475

480

485

gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att 1540

Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile

490

495

500

ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta 1588

Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val

505

510

515

520

aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag 1636

Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln

525

530

535

aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa 1684

Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu

540

545

550

tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg 1732

Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg

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555	560	565	
tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct			1780
Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala			
570	575	580	
gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg			1828
Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu			
585	590	595	600
aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct			1876
Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala			
605	610	615	
caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct			1924
Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala			
620	625	630	
aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att			1972
Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile			
635	640	645	
tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc			2020
Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe			
650	655	660	
ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att			2068
Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile			
665	670	675	680

ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt 2116
 Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu

685 690 695

aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac 2164
 Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp

700 705 710

ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg 2212
 Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg

715 720 725

cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca 2260
 Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser

730 735 740

gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta 2308
 Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val

745 750 755 760

gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct 2356
 Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala

765 770 775

gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg 2404
 Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu

780 785 790

agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga 2452
 Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg
 795 800 805

gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt 2500
 Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu
 810 815 820

atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat 2548
 Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp
 825 830 835 840

aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc 2596
 Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile
 845 850 855

cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt 2644
 Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser
 860 865 870

cat acg tta agt aga tct aca act cat ttg ata tgaagcgtta ccaaaatctt 2697
 His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
 875 880

aaattataga aatgtataga cacctcatatc tcaaataaga aactgactta aatggtactt 2757

gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga 2817

tttttcttct tgaaagagta aggtttacct gttacatttt caagttaatt catgtaaaaa 2877

atgatagtga ttttgatgta atttatctct tgtttgaatc tgtcattcaa aggccaataa 2937

tttaagttgc tatcagctga tattagtagc tttgcaaccc tgatagagta aataaatttt 2997

atgggcggggt gccaaatact gctgtgaatc tatttgtata gtatccatga atgaatttat 3057

ggaaatagat atttgtgcag ctcaatttat gcagagatta aatgacatca taatactgga 3117

tgaaaacttg catagaattc tgattaaata gtgggtctgt ttcacatgtg cagtttgaag 3177

tatttaaata accactcctt tcacagttaa ttttcttctc aagcgttttc aagatctagc 3237

atgtggattt taaaagattt gccctcatta acaagaataa catttaaagg agattgtttc 3297

aaaatatttt tgcaaattga gataaggaca gaaagattga gaaacattgt atattttgca 3357

aaaacaagat gttttagct gtttcagaga gagtacggta tatttatggt aattttatcc 3417

actagcaaat cttagtttag tttgatagtg tgtggaattt tattttgaag gataagacca 3477

tgggaaaatt gtggtaaaga ctgtttgtac cttcatgaa ataattctga agttgccatc 3537

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cttataatta aatgtaaaat tgaaaattca tttgctgttt caaagtgtga tatctttcac 3657

aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717

tatttcctat ttccttaggg agtgctacaa atgtttgtca cttaaatttc aagtttctgt 3777

tttaatagtt aactgactat agattgtttt ctatgccatg tatgtgccac ttctgagagt 3837

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atacctaataa ccc 3910

<210> 53

<211> 622

<212> PRT

<213> Homo sapiens

<400> 53

Met Glu Gly Pro Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly

1 5 10 15

Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn

20 25 30

Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser

35 40 45

Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg

50 55 60

Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys

65 70 75 80

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Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp

85

90

95

Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly

100

105

110

Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His

115

120

125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu

130

135

140

Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln

145

150

155

160

His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn

165

170

175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys

180

185

190

Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser

195

200

205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala

210

215

220

Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly

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225	230	235	240
Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met			
245	250	255	
Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu			
260	265	270	
Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln			
275	280	285	
Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp			
290	295	300	
Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys			
305	310	315	320
Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg			
325	330	335	
Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu			
340	345	350	
Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe			
355	360	365	
Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile			
370	375	380	

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly
385 390 395 400

Phe Thr Lys Ala Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu
405 410 415

Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu
420 425 430

Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys
435 440 445

Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly
450 455 460

Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met
465 470 475 480

Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
485 490 495

Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln
500 505 510

Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
515 520 525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln
530 535 540

Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys
545 550 555 560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr
 565 570 575

Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys
 580 585 590

Phe Gly Leu Val Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr
 595 600 605

Met Val Phe His Pro Ala Arg Glu Lys Val Leu Arg Ser Val
 610 615 620

<210> 54

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<212> DNA

<213> Homo sapiens

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<222> (104).. (1969)

<400> 54

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gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg 115

Met Glu Gly Pro

1

ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca 163

Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro

5

10

15

20

gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc 211

Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala

25

30

35

aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259

Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp

40

45

50

att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg 307

Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu

55

60

65

gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg 355

Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser

70

75

80

ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt 403

Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe

85

90

95

100

tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat 451

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Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn

105

110

115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc 499

Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val

120

125

130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547

Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu

135

140

145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595

Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile

150

155

160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643

Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val

165

170

175

180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca 691

Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro

185

190

195

gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt 739

Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val

200

205

210

gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga 787

Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly

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215	220	225	
aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat			835
Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp			
230	235	240	
atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac			883
Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn			
245	250	255	260
aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga			931
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg			
	265	270	275
gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc			979
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu			
	280	285	290
ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac			1027
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr			
295	300	305	
ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta			1075
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu			
310	315	320	
gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg			1123
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly			
325	330	335	340

tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt	1171
Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val	
345 350 355	
ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca	1219
Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala	
360 365 370	
gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta	1267
Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu	
375 380 385	
tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct	1315
Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala	
390 395 400	
tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc	1363
Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly	
405 410 415 420	
tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca	1411
Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro	
425 430 435	
tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat	1459
Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr	
440 445 450	

gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat 1507

Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His

455

460

465

cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg 1555

His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp

470

475

480

att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca 1603

Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr

485

490

495

500

ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt 1651

Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys

505

510

515

tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca 1699

Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser

520

525

530

tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg 1747

Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu

535

540

545

ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat 1795

Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His

550

555

560

atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc 1843

Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe

565

570

575

580

atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg 1891

Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val

585

590

595

aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac 1939

Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His

600

605

610

cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa 1989

Pro Ala Arg Glu Lys Val Leu Arg Ser Val

615

620

ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaag tgaagtaaag 2049

atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa 2109

aagttctcaa taaaggcatt acaatttttt aggttttagaa agatggactt ttctgataaa 2169

tcttggcaga catctaaaaa aaaaaccata tttttcacaa gaaaatgcaa gttacttttt 2229

ttggaaataa tactcactga ttatggataa aatggaatat ttcagatac tatattggct 2289

gtttcaaat agtactattc tttaaacttg taatttttgc taagttattt gtctttgttg 2349

tatctataaa tatgtaaaaa atatttaaag agatgtacct gtttgcttt cacacttaat 2409

aaaaaatttt tttttgt

2426

<210> 55

<211> 257

<212> PRT

<213> Homo sapiens

<400> 55

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
1 5 10 15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
20 25 30

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
35 40 45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
50 55 60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
65 70 75 80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
85 90 95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
100 105 110

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Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly
115 120 125

Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly
130 135 140

Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln
145 150 155 160

His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly
165 170 175

Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu
180 185 190

Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala
195 200 205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr
210 215 220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu
225 230 235 240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp
245 250 255

Gly

<210> 56

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10).. (780)

<400> 56

tttcccaag atg gcg tcg aag ata ggt tcg aga cgg tgg atg ttg cag ctg 51

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu

1

5

10

atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99

Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly

15

20

25

30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147

Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg

35

40

45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195

Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala

50

55

60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc 243
 Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe
 65 70 75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac 291
 Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr
 80 85 90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac 339
 Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr
 95 100 105 110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt 387
 Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly
 115 120 125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc 435
 Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser
 130 135 140

acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca 483
 Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser
 145 150 155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca 531
 Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro
 160 165 170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg 579
 179/735

Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu

175

180

185

190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627

Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile

195

200

205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675

Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val

210

215

220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723

Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys

225

230

235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771

Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala

240

245

250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc 820

Thr Asp Gly

255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttattt atgctttttg 880

gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca 940

tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000

cagggtttttt tcctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060
 gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120
 aaggaagatg gagattggaa gtgagcaaatt gtgaaaaatt cctctttgaa cctggcagat 1180
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 gtggatcagg cccaggaagg gcacaggggc tgagcactac agaagtcaca tgggttctca 1300
 gggatatcca ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360
 accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420
 tgctgtctct gtttctagct ccatggttgg cctggtgggg gtggagttcc ctcccaaaca 1480
 ccagaccaca cagtcctcca aaaataaaca ttttatatag 1520

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln

1

5

10

15

Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys

	20		25		30
Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu					
	35		40		45
Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe					
	50		55		60
Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile					
	65		70		75
					80
Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His					
	85		90		95
Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val					
	100		105		

<210> 58

<211> 1496

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9).. (329)

<400> 58

ctaccagg atg gct ctc ttc gct ggt ggc aaa ctg cgt gtg cat ctc gac 50

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp

1

5

10

atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98

Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys

15

20

25

30

gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146

Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln

35

40

45

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194

Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu

50

55

60

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242

Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp

65

70

75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg 290

Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met

80

85

90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc 339

Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val

95

100

105

tttgatgac ccttcctttt tacctcattt atttggtact ttccccacac agtcctttat 399

ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459

caaaccattc agatcagcca ctgtctgacc ctggttctta aggacacatg acattagtcc 519

aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaaccga ggactcagtc 579

ctgcttcttt tgctcagagt gattttcttc tgttttcac taaataagca aatgaaaact 639

ctctccatta cttctgctt tctctttgtc cacttacgca gtaggtgact ggcatgtgcc 699

acagagcagg cctgcctca ctgtctgtg gtcagttctg ggttcactta atggctttgt 759

gaatgtaaat aaggggcagg tcttggccct agaggattga gatgtttttc tatacttag 819

aactatTTTT ggataaatta tatatTTTcc ttcttagtag aagtgttact gcctgtaact 879

agctcaaaaat accaatgcag tttctgcatt ctgggttttg ttttctttt ttttttttt 939

ttttttgagt ttgctcttg tcgccaggc tggagtgcaa tggcgtgatc tcagctcact 999

ggcaacatct gcctcccggg ttcaaatgat tctctgcct cagtctcctg agtagctggg 1059

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taccatgttg gccaggctgg tcttagactc ctgacctcag ttgatccacc tgcctcagcc 1179

tctgcattca gtttattcac atatTTTTgg taactcccat ggcagctcct aggatttcag 1239

cggtctgtgg gccagaaagc aggcaccagg gctgacctca aggccgtatc agagggccaa 1299

gcagagttct tttggatacc tgcttttcat cccacagggc cttagagtca gaggtaaggt 1359

agcaacagag ctagaatggg gcaatgcact cttaccctcc ttctcaactt ttatttaagc 1419

tgtgctaaat gttttcttca agggaaccag atttagttct ttacagaatt ttccagttaa 1479

ataaaacatg ttgtaat 1496

<210> 59

<211> 272

<212> PRT

<213> Homo sapiens

<400> 59

Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly

1 5 10 15

Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp

20 25 30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met

35 40 45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly

50 55 60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln

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65	70	75	80
Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr			
	85	90	95
Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr			
	100	105	110
Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys			
	115	120	125
Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg			
	130	135	140
Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu			
145		150	155
His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro			
	165	170	175
Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val			
	180	185	190
Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr			
	195	200	205
Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu			
	210	215	220

Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln
 225 230 235 240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu
 245 250 255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
 260 265 270

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (117)..(932)

<400> 60

atggtaacgg ctcggaagcc taggaggctg ggccggaggg aggcggagga accggtgttc 60

gccgccgccg ctgcttcagc ttattccttg tggcctctgc gggtcctgcc tcagcc atg 119

Met

1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167

Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro

5

10

15

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tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215
 Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val

20 25 30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263
 Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met

35 40 45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311
 Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile

50 55 60 65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359
 Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly

70 75 80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407
 Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu

85 90 95

ggt gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455
 Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr

100 105 110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503
 Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val

115 120 125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551
Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu
130 135 140 145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599
Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His
150 155 160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647
Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser
165 170 175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695
Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu
180 185 190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac 743
Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr
195 200 205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg 791
Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met
210 215 220 225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat 839
His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr
230 235 240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga 887
189/735

Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg

245

250

255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa 932

Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu

260

265

270

taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatttgta 992

aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct 1052

taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgactg 1112

tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172

aaattatcac aaagtgggac ctcagcagta gtgatgtgtg tgtctcatga gcagtgagca 1232

cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca 1292

aatcccaatg ccttgtagct ttcataggat tcctgatcat gcatgttgat gtactggctc 1352

ttcactttgg gctttctgat gttattcac acctttggag agttgcaact tgccacatac 1412

gaaattagtc tcatagtgtg gtgaacttca accccaaaat tttaaaaatg tatttcccc 1472

cagttttaaa ttgcctttga aatttaaaaa aaaaaattta gacttagtac cagaaccaa 1532

aatacctaga tttttggaga acttattaca tacatagaaa catgaatatg gtttaccwct 1592

gtgtgtgtgt gtgtgtgtgt gtgtatacag actttttttt ttaacttggt gattcagatg 1652

tcttggtccc tgaatagtc tagattactt attttgagaa ttgattgtta aaaattacag 1712

ggaattaaata taattgcctt ttttttttta gagggtaaga gatgggtaga agagtatgcc 1772

tctgaaaatt ttattagttt attcttgtgg agaataccaa gaaaatgtgt attgccccat 1832

tgctaaatat gatatatgcc attttgtatt tatttgtccc aagtgtcttt ttttaagagg 1892

agaataaaca ataaggaatt actg 1916

<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser

1 5 10 15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp

20 25 30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln

35 40 45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys

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50	55	60
Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp		
65	70	75
Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile		
85	90	95
Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly		
100	105	110
Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile		
115	120	125
Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu		
130	135	140
Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu		
145	150	155
Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala		
165	170	175
Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile		
180	185	190
Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val		
195	200	205

Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser

210

215

<210> 62

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49).. (705)

<400> 62

gttttctggt tttgctctag tgtttgggtt tcttcgcggc tgctcaag atg aac cga 57

Met Asn Arg

1

ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac 105

Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp

5

10

15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153

Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile

20

25

30

35

tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag 201

Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys

40

45

50

atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga 249
Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg

55

60

65

gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc 297
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala

70

75

80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu

85

90

95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu

100

105

110

115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu

120

125

130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu

135

140

145

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537
Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu

150

155

160

gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac 585
 Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp
 165 170 175

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633
 Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly
 180 185 190 195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681
 Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe
 200 205 210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta 735
 Gly Leu Pro Gln Ile Pro Ala Ser
 215

aaacaaacac atattatggg actaggaaat atttatcttt ccaaattgc cataacagat 795

ttaggtttct ttcctttctt tgaaggaaag ttttaattaca ttgctctttt attttttcca 855

ttaagagact cattgcttgg gaaatgcttt cttcgtacta aaatttgatt cctttttttt 915

cttatgaaaa acgaactcag tttaaaagta ttttagctc gtatgacttg ttttcattca 975

ttaataataa ttigaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa 1035

ctctacagtc tcaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095

ttcatattat gattcagaat cattttctat tgtggtatta taggttggtt aaagtgatgg 1155

cctttttgat gggttttggt gtgtcttgtg aacaagtcgt tactgtgtcc attattggaa 1215

tggaattatc actactgtat catgagtggg tattttgatt ctatggttcc ctcagtatta 1275

catcttgact tgtaatcaat tatgaatatt tcttgatatt taatgtatag gacatttatt 1335

tataactcaat aaatattttt caaaagg 1362

<210> 63

<211> 622

<212> PRT

<213> Homo sapiens

<400> 63

Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro

1 5 10 15

Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly

20 25 30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr

35 40 45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg

50 55 60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn

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65	70	75	80
Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val			
	85	90	95
Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp			
	100	105	110
Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser			
	115	120	125
Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp			
	130	135	140
Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln Phe Gly His Thr			
145	150	155	160
Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met			
	165	170	175
Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His			
	180	185	190
Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn			
	195	200	205
Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu			
210	215	220	

Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn
225 230 235 240

Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys
245 250 255

Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln
260 265 270

Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp
275 280 285

Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile
290 295 300

Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile
305 310 315 320

Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser
325 330 335

Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile
340 345 350

Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe
355 360 365

Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn
370 375 380

Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro
385 390 395 400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu
405 410 415

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
420 425 430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
435 440 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
450 455 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
465 470 475 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
485 490 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
500 505 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
515 520 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
199/735

530

535

540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg

545

550

555

560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe

565

570

575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys

580

585

590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr

595

600

605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val

610

615

620

<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(1879)

<400> 64

atttaacacc aag atg gcg gac ggc ccg gat gag tac gat acc gaa gcg 49

200/735

Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala

1

5

10

ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97

Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His

15

20

25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat 145

Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp

30

35

40

gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat 193

Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr

45

50

55

60

gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg 241

Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro

65

70

75

gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga 289

Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg

80

85

90

ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa 337

Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln

95

100

105

ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa 385

Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln

110	115	120	
ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct 433			
Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro			
125	130	135	140
tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag 481			
Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln			
	145	150	155
ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat 529			
Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp			
	160	165	170
gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca 577			
Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala			
	175	180	185
tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat 625			
Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn			
190	195	200	
gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat 673			
Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His			
205	210	215	220
tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa 721			
Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu			
	225	230	235

gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt	769
Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu	
240 245 250	
gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa	817
Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln	
255 260 265	
gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag	865
Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys	
270 275 280	
ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct	913
Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro	
285 290 295 300	
ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat	961
Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp	
305 310 315	
tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta	1009
Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val	
320 325 330	
cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg	1057
Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu	
335 340 345	

ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg 1105
 Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp
 350 355 360

ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca 1153
 Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro
 365 370 375 380

ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg 1201
 Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp
 385 390 395

aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag 1249
 Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys
 400 405 410

aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc 1297
 Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe
 415 420 425

tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt 1345
 Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly
 430 435 440

gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg 1393
 Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val
 445 450 455 460

ggc aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta 1441

Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu

465

470

475

ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct 1489

Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser

480

485

490

tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg 1537

Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp

495

500

505

aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg 1585

Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met

510

515

520

ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta tta ctc atg 1633

Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met

525

530

535

540

tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga 1681

Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg

545

550

555

atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca acg tct att 1729

Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile

560

565

570

gaa agc cca ttc aac cat gga tgt gta aga aat att ata gac ttc ttt 1777

Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe

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575

580

585

gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc 1825

Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr

590

595

600

agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag 1873

Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln

605

610

615

620

ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgggtg cctgaaaatt 1929

Leu Val

gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989

tgtagggcta atggtgaatt ttacagtctt tttttcaaca cttttattaa caaaagtaaa 2049

catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109

ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct cacagtattt 2169

ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat cagaaatggt 2229

cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc agtctagtag 2289

gagtattgca tctaattcca ggagcattgt tttaagttga ttgactagtt attatgtaca 2349

tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc tactgtgatg 2409

ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca atgttttggt 2469
 tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt gtagtaacct 2529
 tactctgagg ttttacggtc tgataatgaa gcacttgcac gagtatagta agtcatgttt 2589
 ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa tgtatactag 2649
 cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagttccat 2709
 ttttaagggt taagggtgta ttttcaagaa aaggcagaac aaataatgca aaattctcag 2769
 taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata attgtagaca 2829
 aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889
 agaaaagctg acagtatatt ctggtttcaa taaatgacc tatcagaaag tagaatttc 2948

<210> 65

<211> 632

<212> PRT

<213> Homo sapiens

<400> 65

Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp

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10

15

Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu

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	20		25		30										
Ile	Lys	Pro	Gln	Ser	His	Tyr	Asn	His	Gly	Tyr	Gly	Glu	Pro	Leu	Gly
	35		40		45										
Arg	Lys	Thr	His	Ile	Asp	Asp	Tyr	Ser	Thr	Trp	Asp	Ile	Val	Lys	Ala
	50		55		60										
Thr	Gln	Tyr	Gly	Ile	Tyr	Glu	Arg	Cys	Arg	Glu	Leu	Val	Glu	Ala	Gly
	65		70		75										
Tyr	Asp	Val	Arg	Gln	Pro	Asp	Lys	Glu	Asn	Val	Thr	Leu	Leu	His	Trp
			85		90									95	
Ala	Ala	Ile	Asn	Asn	Arg	Ile	Asp	Leu	Val	Lys	Tyr	Tyr	Ile	Ser	Lys
			100		105									110	
Gly	Ala	Ile	Val	Asp	Gln	Leu	Gly	Gly	Asp	Leu	Asn	Ser	Thr	Pro	Leu
			115		120									125	
His	Trp	Ala	Thr	Arg	Gln	Gly	His	Leu	Ser	Met	Val	Val	Gln	Leu	Met
			130		135									140	
Lys	Tyr	Gly	Ala	Asp	Pro	Ser	Leu	Ile	Asp	Gly	Glu	Gly	Cys	Ser	Cys
			145		150					155				160	
Ile	His	Leu	Ala	Ala	Gln	Phe	Gly	His	Thr	Ser	Ile	Val	Ala	Tyr	Leu
			165		170									175	

Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr
180 185 190

Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg
195 200 205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His
210 215 220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val
225 230 235 240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile
245 250 255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp
260 265 270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn
275 280 285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys
290 295 300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile
305 310 315 320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly
325 330 335

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His
340 345 350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe
355 360 365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe
370 375 380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr
385 390 395 400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr
405 410 415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser
420 425 430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val
435 440 445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp
450 455 460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg
465 470 475 480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met
210/735

	485	490	495
Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr			
	500	505	510
Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser			
	515	520	525
Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp			
	530	535	540
Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly			
545	550	555	560
Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys			
	565	570	575
Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg			
	580	585	590
Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro			
	595	600	605
Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile			
610	615	620	
Ser Gly Ser Gly Tyr Gln Leu Val			
625	630		

<210> 66

<211> 4715

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (108).. (2003)

<400> 66

gaagaaggag gaggaggccc gcgtcgcctc cggcggggct cgcgctcgcc ccgcgctcgc 60

cctcgcctc gcccgagccc cgggagggtg aaacgctttc tcccagc atg cag cgg 116

Met Gln Arg

1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat 164

Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp

5

10

15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212

Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro

20

25

30

35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260

Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr

40

45

50

cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat 308
His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr

Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val

cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc 404
Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att 452
Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile
100 105 110 115

gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc 500
Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala
120 125 130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt 548
Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly
135 140 145

gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg 596
Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu
150 155 160

gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa 644

Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys

165

170

175

gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg 692

Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met

180

185

190

195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta 740

Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu

200

205

210

aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act 788

Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr

215

220

225

gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt 836

Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu

230

235

240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa 884

Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu

245

250

255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac 932

Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn

260

265

270

275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc 980

His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe

214/735

280	285	290	
ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta			1028
Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu			
295	300	305	
gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta			1076
Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu			
310	315	320	
aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg			1124
Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp			
325	330	335	
gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat			1172
Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His			
340	345	350	355
agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat			1220
Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr			
360	365	370	
gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc			1268
Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile			
375	380	385	
cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga			1316
His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly			
390	395	400	

aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa 1364
 Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln

405

410

415

aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc 1412
 Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu

420

425

430

435

agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa 1460
 Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys

440

445

450

cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc 1508
 His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys

455

460

465

cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg 1556
 Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met

470

475

480

ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt 1604
 Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly

485

490

495

tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat 1652
 Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp

500

505

510

515

gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg 1700
 Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met
 520 525 530

ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta 1748
 Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val
 535 540 545

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca 1796
 Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr
 550 555 560

aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca 1844
 Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr
 565 570 575

acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata 1892
 Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile
 580 585 590 595

gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg 1940
 Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val
 600 605 610

gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct 1988
 Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser
 615 620 625

ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgggtg 2043
 217/735

Gly Tyr Gln Leu Val

630

cctgaaaatt gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga 2103

gcatgctatg tgtagggcta atgggtgaatt ttacagtctt tttttcaaca cttttattaa 2163

caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

taattttaat gtttcttaat gtggaaattc acaacatact caacttttgg gttttgttct 2283

cacagtattt ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat 2343

cagaaatggt cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc 2403

agtctagtag gagtattgca tctaattcca ggagcattgt ttttaagttga ttgactagtt 2463

attatgtaca tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc 2523

tactgtgatg ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca 2583

atgttttggt tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt 2643

gtagtaacct tactctgagg ttttacggtc tgataatgaa gcacttgcac gagtatagta 2703

agtcatgttt tttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa 2763

tgtatactag cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa 2823

acagttccat ttttaagggt taagggtgta ttttcaagaa aaggcagaac aaataatgca 2883

aaattctcag taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata 2943

attgtagaca aaataatggc atttaactaa agatggagca tgatctaagt acatagcaca 3003

tgtgaataaa agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag 3063

tagaatttca tccccaaagag tatttcagtt tatccaatat tgagtaagtt ctgaaacagt 3123

tttagaaaaa attttctttt tgtaaagt gatgcactga tcaatttttg tcacagcatt 3183

ttcacactt catggtggac tactagtcac tgcttcata aatattgttt acagggtgag 3243

atttggttta ttcacttta gtgctgtagc aaactgtggt tcgagcaacc tgtgggaaat 3303

ctgtgagagg gaatggggtg ggagatgtgg gggaatggtg gtcagactga tgacagatcc 3363

tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctcttt 3423

gtgtctgtgt tagtggtttt aaagctgctc atttcatttt gtccaaccaa aaagaaaagg 3483

gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543

caagttcact gcatgtctga tgcttggtaa aactagtctt cctgtaaaa tgcagattac 3603

aggatattaa gcaatctagt ggtatacccg ccccttgccct tagtaagagg agcagtgaaa 3663

tgtatatagt tgatgttcag tatttccaag taccattttt atatagtagc ttatttgacc 3723

ataagtcaca catcaaaaaa agattaccct tagtgatatgt gttttaatat tagaaaattg 3783

gcatatgtac tttatTTTTg aaaagggaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccattttgtc atagaatgta aaaattgggtt aactttacaa atgtcagcta gttttgacta 3903

ctaattgggg gaaatttttag ataattttta aattcaaagt tatttataaa atgctagaat 3963

ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc atttttatcg 4023

aatacatttt tatcaacagt taaagactat ggtggTTTT tcagagtttg gctaagaatg 4083

ttgttaccat cttctttgtt tgtggtacaa tattttcagt gcaaaagaga tgtcattcag 4143

ttaaaaagac aaacctctag atgtgtaatt acatggaaaa tactagcaat gtgaatgctt 4203

ttgtagtaac catctttag tacctgtgaa atctataact cagaaatggg cagatggcca 4263

ggagccagct atgcagcagt ataccatctg ttttaattatt ttgtaggtcc tgtgtgtgga 4323

accaactata aaccagttc taaagtgtg tatgatgtg aacctttggg aatagttctt 4383

atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443

tacttccttg gagttttttt tcattcatat ttttgttgtt tccaggaatt tatttgatat 4503

taatgggcgt aaaacagcat cattgtactt aagctatgga tgtttttatt ttatatattc 4563

tttatttata actgtgccaa gtattatitt gctacttacc gtgttattct gtggaaagaa 4623

aaacctgtaa agtgtttaat aaattagccc tccttacata aattaaatgt caaaattttg 4683

taaaatatta atcagaataa atactgactc tt 4715

<210> 67

<211> 498

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1 5 10 15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65 70 75 80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

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	85	90	95
Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala			
	100	105	110
Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met			
	115	120	125
Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg			
	130	135	140
Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln			
145	150	155	160
Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp			
	165	170	175
Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly			
	180	185	190
Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln			
	195	200	205
Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn			
	210	215	220
Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile			
225	230	235	240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
245 250 255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
260 265 270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
275 280 285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
290 295 300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305 310 315 320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
325 330 335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
355 360 365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
370 375 380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385 390 395 400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
405 410 415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
420 425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
435 440 445

Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln
450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465 470 475 480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
485 490 495

Ser Cys

<210> 68

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 68

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51

Met Ala Arg Leu Glu Val Ile Glu Leu Pro

1 5 10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99

His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

15 20 25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147

Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

30 35 40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195

Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

45 50 55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243

His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

60 65 70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291

Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu

75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339

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Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro

95

100

105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387

Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg

110

115

120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435

Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu

125

130

135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483

His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly

140

145

150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531

Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn

155

160

165

170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579

Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

175

180

185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627

Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190

195

200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675

Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

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205	210	215	
cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct			723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro			
220	225	230	
ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg			771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu			
235	240	245	250
gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc			819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala			
255	260	265	
cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag			867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys			
270	275	280	
ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac			915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp			
285	290	295	
ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca			963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro			
300	305	310	
gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc			1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu			
315	320	325	330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059
 Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly

335 340 345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107
 Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

350 355 360

cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca 1155
 His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser

365 370 375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203
 Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly

380 385 390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251
 Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp

395 400 405 410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299
 Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg

415 420 425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347
 Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile

430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta 1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu

445

450

455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala

460

465

470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser

475

480

485

490

cag aaa ctt tgg gaa ttc tct tgt tagttgggta gttttactgt aattttctat 1545
Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agtttttggtt tcttcctttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgacctg 1845

atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 69

<211> 498

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1 5 10 15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65 70 75 80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

85 90 95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala

100 105 110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met

115 120 125

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Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg

130

135

140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln

145

150

155

160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp

165

170

175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly

180

185

190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln

195

200

205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn

210

215

220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile

225

230

235

240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala

245

250

255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val

260

265

270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr

231/735

275	280	285
Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro		
290	295	300
Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu		
305	310	315 320
Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu		
	325	330 335
Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu		
	340	345 350
Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr		
	355	360 365
Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr		
	370	375 380
Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser		
385	390	395 400
Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser		
	405	410 415
Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe		
	420	425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
 435 440 445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln
 450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
 465 470 475 480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
 485 490 495

Ser Cys

<210> 70

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 70

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51

Met Ala Arg Leu Glu Val Ile Glu Leu Pro

1 5 10

233/735

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99
 His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

15 20 25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147
 Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

30 35 40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195
 Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

45 50 55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243
 His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

60 65 70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291
 Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu

75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339
 Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro

95 100 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387
 Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg

110 115 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435
 Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
 125 130 135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483
 His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
 140 145 150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531
 Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
 155 160 165 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579
 Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
 175 180 185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627
 Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val
 190 195 200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675
 Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val
 205 210 215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723
 Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
 220 225 230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771
 235/735

Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
 235 240 245 250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819
 Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala
 255 260 265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867
 Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
 270 275 280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915
 Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
 285 290 295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963
 Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro
 300 305 310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011
 Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
 315 320 325 330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059
 Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly
 335 340 345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107
 Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr
 236/735

350	355	360	
cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca			1155
His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser			
365	370	375	
tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc			1203
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly			
380	385	390	
act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac			1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp			
395	400	405	410
ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc			1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg			
415	420	425	
tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc			1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile			
430	435	440	
tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta			1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu			
445	450	455	
cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca			1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala			
460	465	470	

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491

Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser

475

480

485

490

cag aaa ctt tgg gaa ttc tct tgt tagttgggta gttttactgt aattttctat 1545

Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agtttttggt tcttcctttg aattttttat 1605

attcttttctt tctctttttt gtttcttctt ctttgagtat ttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc ttgtttttgt 1725

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggtaag atgattcttt tctgatcctg 1845

atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 71

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His

238/735

1	5	10	15
Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr			
20	25	30	
Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr			
35	40	45	
Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro			
50	55	60	
Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly			
65	70	75	80
Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro			
85	90	95	
Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp			
100	105	110	
Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr			
115	120	125	
Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala			
130	135	140	
Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu			
145	150	155	160

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
165 170 175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly
180 185 190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val
195 200 205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg
210 215 220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly
225 230 235 240

Gln Trp Ile Gln Arg
245

<210> 72

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (127)..(861)

<400> 72

ggaagtcggc caccttcctc cgtcccggcc gttagcccag ccaagcccag ccaagcccag 60

ccaagccccg ccgatcgcg gcaccggagc cagccccgca gcgggtcccg cctgtctgtc 120

acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser

1

5

10

atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216

Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser

15

20

25

30

atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264

Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile

35

40

45

ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac 312

Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His

50

55

60

cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg 360

Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg

65

70

75

ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct 408

Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser

80

85

90

ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc 456

Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile
 95 100 105 110

gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc 504
 Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe
 115 120 125

agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag 552
 Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys
 130 135 140

gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg 600
 Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu
 145 150 155

gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat 648
 Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn
 160 165 170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc 696
 Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile
 175 180 185 190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc 744
 Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly
 195 200 205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att 792
 Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile
 242/735

210

215

220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt 840

Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val

225

230

235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact 891

Leu Gly Gln Trp Ile Gln Arg

240

245

gtcagaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951

ctagggctctg tgaacgaggc ctgtctcttc cctgggggttt ctttccatgg cctttatttc 1011

tcctcttcca gtgggagttt tgcaggctct tctctgtgga aacttcacga gcgttggtctg 1071

ggcctcggct tcgctggagt gtactccagg gtgaaggcag agtgggattt gagaccagg 1131

tagtggagga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191

tcaccgggca tagcctggaa gcccgaagtc tgttctgact ttgcctggct gtctccttga 1251

cccgcctcct agatcattgt ccttgatgtc caggctgggt catttaaaat agagatgcaa 1311

tcaggaaggt tgggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371

tcagcacctg agtcacagcc caggtgcccg gaagcagcct cttcgcatag gcagtgattt 1431

gcgattactt taaagctcac cttttttctt cccctctctg ttcgctgctg tcagcataat 1491

gattgtgttc cttccctatg ggatccatct gttttgtaaa caataaagcg tctgaggag 1551

<210> 73

<211> 352

<212> PRT

<213> Homo sapiens

<400> 73

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

1 5 10 15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu

85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp

244/735

100	105	110
Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu		
115	120	125
Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro		
130	135	140
Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His		
145	150	155
Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly		
165	170	175
Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly		
180	185	190
Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val		
195	200	205
Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln		
210	215	220
Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp		
225	230	235
Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe		
245	250	255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
260 265 270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
275 280 285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
290 295 300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305 310 315 320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
325 330 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
340 345 350

<210> 74

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103).. (1158)

<400> 74

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tatccttggc gccacagtcg gccaccgggg ctcgccgccc tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5

10

15

20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

25

30

35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40

45

50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306

Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile

55

60

65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354

Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val

70

75

80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402

Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys

85

90

95

100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450
 Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile

105 110 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498
 Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

120 125 130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546
 Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val

135 140 145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594
 Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln

150 155 160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642
 Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys

165 170 175 180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690
 Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr

185 190 195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738
 Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro

200 205 210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786
 Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
 215 220 225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834
 Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
 230 235 240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882
 Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
 245 250 255 260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930
 Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
 265 270 275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978
 Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
 280 285 290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026
 Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
 295 300 305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074
 Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
 310 315 320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122
 249/735

Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325 330 335 340

cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg 1168

Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser

345 350

gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468

caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggatgaatcg 1528

ttgcttgctg tggacttggg ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcagggtcaa cttgtgttcc 1708

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tgaagtcagc acatccgctt ctgccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttgccactg gccctgattt 1888
 gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948
 gcgcagaggc ctgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008
 ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068
 tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128
 tcgcttctcc ttgtgttacc cctcccagt attaccattt gccctcacc tgcccttgg 2188
 gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248
 acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcac tctcgtcctc 2308
 ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368
 gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

1

5

10

15

251/735

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
130 135 140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
252/735

	165	170	175
Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly			
	180	185	190
Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val			
	195	200	205
Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln			
	210	215	220
Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp			
225	230	235	240
Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe			
	245	250	255
Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu			
	260	265	270
Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser			
	275	280	285
Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val			
	290	295	300
Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val			
305	310	315	320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys

325

330

335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

340

345

350

<210> 76

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 76

ttaggccggg ggggtgcgt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc 60

tatccttggc gccacagtcg gccaccgggg ctgccgccg tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5

10

15

20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

254/735

25	30	35	
caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag			258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys			
40	45	50	
agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata			306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile			
55	60	65	
gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg			354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val			
70	75	80	
gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag			402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys			
85	90	95	100
atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc			450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile			
105	110	115	
att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag			498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu			
120	125	130	
gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg			546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val			
135	140	145	

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594
 Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln

150

155

160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642
 Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys

165

170

175

180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690
 Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr

185

190

195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738
 Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro

200

205

210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786
 Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser

215

220

225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834
 Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala

230

235

240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882
 Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg

245

250

255

260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930
 Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
 265 270 275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978
 Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
 280 285 290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026
 Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
 295 300 305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074
 Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
 310 315 320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122
 Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg
 325 330 335 340

cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg 1168
 Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
 345 350

gaagccgcac agcttgacct ggaagcacc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468

caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggatgaatcg 1528

ttgcttgctg tggacttggg ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcagggtcaa cttgtgttcc 1708

tttccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

tgaagtcagc acatccgctt ctgccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagagga ctcgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc cctcccagt attaccatctt gccctcacc tgcccttggg 2188

gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcac tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 77

<211> 697

<212> PRT

<213> Homo sapiens

<400> 77

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala

1 5 10 15

Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser

20 25 30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile

35 40 45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile

50 55 60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile

65 70 75 80

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Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn
85 90 95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser
100 105 110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu
115 120 125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser
130 135 140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu
145 150 155 160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys
165 170 175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile
180 185 190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe
195 200 205

Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile
210 215 220

Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp
260/735

225 230 235 240

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu

245 250 255

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met

260 265 270

Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr

275 280 285

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe

290 295 300

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His

305 310 315 320

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp

325 330 335

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe

340 345 350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala

355 360 365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser

370 375 380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe
385 390 395 400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile
405 410 415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu
420 425 430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu
435 440 445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly
450 455 460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys
465 470 475 480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp
485 490 495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp
500 505 510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp
515 520 525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu
530 535 540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn
545 550 555 560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp
565 570 575

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp
580 585 590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys
595 600 605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp
610 615 620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met
625 630 635 640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp
645 650 655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys
660 665 670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr
675 680 685

Gly Gln Gly Phe Lys Leu Val Lys Ser
263/735

690

695

<210> 78

<211> 3008

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (372).. (2462)

<400> 78

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aaagtttacg cgcacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcgggt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc 410

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu

1

5

10

tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458
Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met
15 20 25

gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554
Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn
50 55 60

gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650
Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser
80 85 90

gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat 746
Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr
110 115 120 125

Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu
130 135 140

aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt 842
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val
145 150 155

gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg 890
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu
160 165 170

gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg 938
Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met
175 180 185

ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta 986
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu
190 195 200 205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa 1034
Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys
210 215 220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct 1082
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro
225 230 235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa 1130
Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys
266/735

240	245	250	
ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt	1178		
Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe			
255	260	265	
gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt	1226		
Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu			
270	275	280	285
aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt	1274		
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe			
290	295	300	
gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg	1322		
Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp			
305	310	315	
gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac	1370		
Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His			
320	325	330	
agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg	1418		
Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met			
335	340	345	
cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt	1466		
Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu			
350	355	360	365

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att 1514
 Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile

370 375 380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat 1562
 Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His

385 390 395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga 1610
 Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly

400 405 410

tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca 1658
 Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro

415 420 425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act 1706
 Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr

430 435 440 445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag 1754
 Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu

450 455 460

acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg 1802
 Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu

465 470 475

cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc 1850
 His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro

480

485

490

aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca 1898
 Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr

495

500

505

gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt 1946
 Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu
 510 515 520 525

ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att 1994
 Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile

530

535

540

atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg 2042
 Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg

545

550

555

aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa 2090
 Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys

560

565

570

aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca 2138
 Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr

575

580

585

aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186

Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp
590 595 600 605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234
Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg
610 615 620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282
Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
625 630 635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330
His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
640 645 650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378
Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
655 660 665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426
Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val
670 675 680 685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac 2472
Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
690 695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532

gtatgctgta tttttatttg tggaaaatac ctgctactt ctgtagctgc tctcactttg 2592

tcttttctta agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa 2652

gtatgtaggg agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712

ctttcaggaa tgtttgctta tggctctgat tagaaagaaa cagttgtcta tgctctgcaa 2772

tggccaatga tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat 2832

gtagaccaga taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt 2892

cttttttcca aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct 2952

tagaaaagaa agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac 3008

<210> 79

<211> 611

<212> PRT

<213> Homo sapiens

<400> 79

Met Glu Ala Ala Ser Leu Ser Leu Ser Asn Leu Trp Phe Gly Phe Leu

1 5 10 15

Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val

20 25 30

Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg
35 40 45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg
50 55 60

Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala
65 70 75 80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu
85 90 95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser
100 105 110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe
115 120 125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe
130 135 140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu
145 150 155 160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys
165 170 175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe
180 185 190

Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val
195 200 205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile
210 215 220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys
225 230 235 240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg
245 250 255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln
260 265 270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser
275 280 285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
290 295 300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
305 310 315 320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe
325 330 335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln
273/735

340	345	350
Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe		
355	360	365
Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser		
370	375	380
Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu		
385	390	395
400		
Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr		
405	410	415
Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp		
420	425	430
Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly		
435	440	445
Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr		
450	455	460
Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val		
465	470	475
480		
Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro		
485	490	495

Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn
500 505 510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala
515 520 525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro
530 535 540

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile
545 550 555 560

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu
565 570 575

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met
580 585 590

Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu
595 600 605

Val Lys Ser
610

<210> 80

<211> 3007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (629).. (2461)

<400> 80

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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttcccca 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggttttggtt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcgggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta catgtgtaaa tcaactgcgtt attgctttag tcattgtctc tatttagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggatatctg 480

ctatttagcc agaatcaatt tattggttgc tatatgctta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc 652

Met Glu Ala Ala Ser Leu Ser Leu

tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700
 Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp

10

15

20

aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748
 Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu

25

30

35

40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796
 Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg

45

50

55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844
 Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu

60

65

70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892
 Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val

75

80

85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940
 Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu

90

95

100

att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt 988
 Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val

105

110

115

120

att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat 1036
 Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn
 125 130 135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc 1084
 Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe
 140 145 150

ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc 1132
 Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro
 155 160 165

ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct 1180
 Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala
 170 175 180

gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga 1228
 Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg
 185 190 195 200

gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga 1276
 Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly
 205 210 215

att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga 1324
 Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly
 220 225 230

ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg 1372
 278/735

Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg
235 240 245

aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc 1420
Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg
250 255 260

cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca 1468
His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala
265 270 275 280

aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc 1516
Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe
285 290 295

ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg 1564
Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly
300 305 310

ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat 1612
Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr
315 320 325

gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca 1660
Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr
330 335 340

ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc 1708
Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly
279/735

345	350	355	360	
atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc				1756
Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr				
	365	370	375	
tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat				1804
Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His				
	380	385	390	
tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga				1852
Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg				
	395	400	405	
cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga				1900
His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly				
	410	415	420	
gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata				1948
Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile				
425	430	435	440	
gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc				1996
Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile				
	445	450	455	
gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa				2044
Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys				
	460	465	470	

att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca 2092
 Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr

475

480

485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa 2140
 Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys

490

495

500

gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act 2188
 Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr

505

510

515

520

gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg 2236
 Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp

525

530

535

agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac 2284
 Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His

540

545

550

tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca 2332
 Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala

555

560

565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt 2380
 Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe

570

575

580

agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg 2428

Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu

585

590

595

600

gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481

Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

605

610

gatattaata agcactcata ctaccaatta tcactaactt gccatTTTTT gtatgctgta 2541

TTTTtatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg tcttttctta 2601

agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa gtatgtaggg 2661

agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa 2721

tgtttgctta tggctctgat tagaaagaaa cagttgtcta tgctctgcaa tggatcaatga 2781

tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat gtagaccaga 2841

taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt cttttttcca 2901

aacagtaggt ttcaccaag accatttgaa gaactgcaaa ctctttctct tagaaaagaa 2961

agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac 3007

<210> 81

<211> 184

<212> PRT

<213> Homo sapiens

<400> 81

Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu

1 5 10 15

Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln

20 25 30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys

35 40 45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln

50 55 60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser

65 70 75 80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu

85 90 95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro

100 105 110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys

115 120 125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser

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130

135

140

Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile

145

150

155

160

Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro

165

170

175

Thr Glu Met Asp Glu Asn Glu Ser

180

<210> 82

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (285)..(836)

<400> 82

tttttacaaa ggccccgggc gcgagaggac gtgctctgcc agccagtggg aaggcaggcc 60

gcgcgcgcgg gagcgcggga ggatcggcgg ctgcggtca ctggtccctg gctcggttcc 120

ccgcacccccg gggctcacac ttaccgcgc gcgaggagcag cggccgggtg tccaccccca 180

tctgcgccc agtctctctg attcccctcg ctctgagccg ggagagccga acagctgaag 240

agagttcact gactccccag ccccaggtgg gccttgtgca catc atg acc agt ttt 296

Met Thr Ser Phe

1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344

Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val

5

10

15

20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392

Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe

25

30

35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440

Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn

40

45

50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488

Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val

55

60

65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc 536

Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser

70

75

80

ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc 584

Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser

85

90

95

100

aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg 632
 Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met
 105 110 115

gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag 680
 Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu
 120 125 130

tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc 728
 Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu
 135 140 145

ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc 776
 Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly
 150 155 160

act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat 824
 Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp
 165 170 175 180

gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa 876
 Glu Asn Glu Ser

gagctctgta gatgctgtat agacactaaa taagagttga ttagggtagt atattatagt 936

catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaattgtg 996

ttagtcatta acttagtcac ctgttgatt ctggatctac acaaaattat tttactgct 1056

cttattaatc tgtgaggatt aatatacaaa aagtatcctt tgagatgaag tcgtgttctc 1116
 aaaataaggt tatattatctt tctttttctg cttgattttc atcttgtgtt ttgctttgtt 1176
 tttgtaagga accatctctt ggtttggtca catcagttca caacagccat ttgttttcaa 1236
 ggtcaaggct ccaggcaggt tgttactggt gtttgcagcc tgtcagtact tgcagtactg 1296
 gaataggttc taggctagtg tctgcgcgtc actgtgggtt tagcatggga ggacttattt 1356
 gagaaatact accttacttt tctatgattt ctttttacag agttatagtg tgtttactcc 1416
 taagatgaca gttctctttg tctatattca gcatctaaga caaatattta aacattttta 1476
 agaaccactg tgtaaagttt aggattattt acttaccaaa ttagaagttt gacttttatg 1536
 tgttatacac aatcttaaaa tttcacgaat tcaccttttt aatagtatcc atgtacataa 1596
 taaaatcaaa gtttaattag c 1617

<210> 83

<211> 392

<212> PRT

<213> Homo sapiens

<400> 83

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1

5

10

15

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Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
85 90 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
288/735

165	170	175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser		
180	185	190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser		
195	200	205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met		
210	215	220
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr		
225	230	235 240
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser		
245	250	255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu		
260	265	270
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr		
275	280	285
Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu		
290	295	300
Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly		
305	310	315 320

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala

325

330

335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val

340

345

350

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

355

360

365

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370

375

380

Val Glu Ser Pro Val Gln Lys Val

385

390

<210> 84

<211> 1898

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1294)

<400> 84

acttcgctg gccgctggct cgctggccgc tcctggaggc ggcggcggga gcgcaggggg 60

cgcgcgggccc ggggactcgc attccccggt tccccctcca cccacgcgg cctggacc 118

290/735

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc	166
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser	
1 5 10 15	
cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc	214
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr	
20 25 30	
cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc	262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser	
35 40 45	
ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac	310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn	
50 55 60	
tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt	358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys	
65 70 75 80	
gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc	406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro	
85 90 95	
cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg	454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu	
100 105 110	

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc 982
 Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
 275 280 285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc 1030
 Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
 290 295 300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078
 Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
 305 310 315 320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126
 Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
 325 330 335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174
 Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
 293/735

340

345

350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga 1222

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

355

360

365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370

375

380

gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt 1324

Val Glu Ser Pro Val Gln Lys Val

385

390

gaaataggac cctcccacca tccccttctg ctgtaacctc tgaggggagct ggctgaaagg 1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc 1444

ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agttttattct 1504

gagccccggg ggtagacagt cctcagttag gggttttggg gagtttgggg tcaagagagc 1564

ataggtaggt tccacagtta ctcttccac aagttccctt aagtcttgcc ctagctgtgc 1624

tctgccacct tccagactca ctcccctctg caaataacct catttcttac cctggtgaga 1684

aaagcacaag cgggtgtaggc tccaatgctg ctttcccagg aggggtgaaga tgggtgctgtg 1744

ctgaggaaag gggatgcaga gccctgccca gcaccaccac ctctatgct cctggatccc 1804

taggctctgt tccatgagcc tgttcaggt tttggtactt tagaaatgta actttttgct 1864

cttataattt tattttatta aattaaatta ctgc 1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85 90 95

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Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
165 170 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
180 185 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
195 200 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
210 215 220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225 230 235 240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
296/735

	245	250	255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu			
	260	265	270
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp			
	275	280	285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe			
	290	295	300
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu			
305	310	315	320
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu			
	325	330	335
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln			
	340	345	350
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr			
	355	360	365
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu			
	370	375	380
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val			
385	390	395	400

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
405 410 415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
420 425 430

<210> 86

<211> 2018

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (1414)

<400> 86

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cgcgcgggccc ggggactcgc attccccggt tccccctcca cccacgcgg cctggacc 118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
 100 105 110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 300/735

260

265

270

atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg 982

Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp

275

280

285

cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt 1030

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe

290

295

300

ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa 1078

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu

305

310

315

320

cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag 1126

Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu

325

330

335

ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag 1174

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln

340

345

350

ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc 1222

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr

355

360

365

atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt 1270

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu

370

375

380

301/735

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg 1318

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val

385

390

395

400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag 1366

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys

405

410

415

caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt 1414

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val

420

425

430

tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tccccttctg 1474

ctgtaacctc tgagggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca 1534

gaccagctct gcagcagggg attggggagc ccaggaggca gccttcctt ttgccttaag 1594

tcacccatct tccagtaagc agtttattct gagccccggg ggtagacagt cctcagtgag 1654

gggttttggg gagtttgggg tcaagagagc ataggtaggt tccacagtta ctcttccac 1714

aagttccctt aagtcttgcc ctagctgtgc tctgccacct tccagactca ctcccctctg 1774

caaataacctg catttcttac cctggtgaga aaagcacaag cgggtgtaggc tccaatgctg 1834

ctttcccagg aggggtgaaga tgggtgctgtg ctgaggaaag gggatgcaga gccctgcca 1894

gcaccaccac ctcctatgct cctggatccc taggctctgt tccatgagcc tgttgcaggt 1954

tttggtaactt tagaaatgta acttttttgc tttataattt tattttatta aattaaatta 2014

ctgc

2018

<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser

1

5

10

15

Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser

20

25

30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His

35

40

45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser

50

55

60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys

65

70

75

80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val

303/735

	85	90	95
Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe			
	100	105	110
Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala			
	115	120	125
Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu			
	130	135	140
Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser			
145	150	155	160
Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu			
	165	170	175
Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile			
	180	185	190
Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg			
	195	200	205
Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu			
	210	215	220
Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala			
225	230	235	

<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (111).. (815)

<400> 88

aaaaggaaga cagaaaagcc gcgggctgac tgtggtggcg ctgcctgca gattgaaaag 60

aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt 116

Met Gly

1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt 164

Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly

5

10

15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc 212

Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser

20

25

30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat 260

Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn

35

40

45

50

aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa 308
 Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu
 55 60 65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg 356
 Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val
 70 75 80

ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat 404
 Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn
 85 90 95

ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag 452
 Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu
 100 105 110

atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat 500
 Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn
 115 120 125 130

ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat 548
 Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp
 135 140 145

act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac 596
 Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn
 150 155 160

agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat 644
 306/735

Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn

165

170

175

ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc 692

Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala

180

185

190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt 740

Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe

195

200

205

210

cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga 788

Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg

215

220

225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat 835

Asn Met Val Gln Arg Gln Phe Ile Ala

230

235

gtggctggct cttgttttgt aaaccaaagtg attaatcttc acttgagaaa gcagtttcta 895

ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955

taaatttctg caggacagcc tataaaattg tggactttt tgatgtttca gtaaacttga 1015

cattgtcaga gtttcaagga cttttctttc acaattttcc tagttcatgg atatgaaaaa 1075

ggaatttctca atccatattc cttgtattga accttgaaca aaaacttgta tgacagacat 1135

ttttaaaaat gtgacaacac ttttattctc tgaattttga tctcaaagga cacagaaaaa 1195

aatggcccc aggagatctg atcacacttc ctctgaggc acctctcatg gatgttgcaa 1255

taagcattcg ggtactatca cccagaaata tgaattgcc aatagaaca tttagcatgt 1315

taagcgttga tgcataaaa atcagaaata gatgtgagaa tggtggaact tttaaaaga 1375

accagtcaa atgtattttc tgctgaaatc tgcataattg gaggcatttc ccaccaccga 1435

ttcacagccc atttgatagt gtggtagtta gggacttcgt ggagtgggtg tcagacgtcc 1495

cctggggcct aaatctcttc atattagtca tcatttgtaa ctatggcttt attgcagag 1555

cttctaaaag gcgtataact gtgtgagtgg ccagatattc actttttaga tcaaaaacct 1615

ctcttatgga agctttaaaa gtttccgtca cacacaattc tcttctcagg aagtatttct 1675

catttaggtc ttcaaagtag cctgactgtg tgcattgtg tgtgtgatag gttatttata 1735

aagactttgg atagaaggag atgtatttta ttacctcta ttctagagcc catgctcct 1795

aacaagccag agaggcccca aacaggattg tttctttcct ccacagccct tctgcccac 1855

tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggcatgtc 1915

atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgcc 1975

ctgaggatga atgtaactgt gggcaaacta tttaccctcc tttatctgtg aaatgaaagg 2035

gttgaattga tggatctcta aaggcttttg tcctctatga ggatgtgaaa aactagggac 2095
 cacaaaaggg aacaagcaaa aaagtttggg ttcgataaag tgatatgtaa tagttgcaga 2155
 aggctttata tatgcttata atgaaaagat attttttgta tattgacagc ataatttatt 2215
 tttaatgctg tcattacact taaagtcaca ggaaaaaaat atacatgctt actcaggctt 2275
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 agtattcatt tttttgccat aatgcttcct gtaaagccaa ttttatatac taataaaaca 2635
 tgaactgccc actcttcatg cctgccaaac ttggggcaat tgatgctaaa tgggtattttt 2695
 aaaataaatg tttttattct tt 2717

<210> 89

<211> 245

<212> PRT

<213> Homo sapiens

<400> 89

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys

1 5 10 15

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20 25 30

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35 40 45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50 55 60

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65 70 75 80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85 90 95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

100 105 110

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

115 120 125

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

130 135 140

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Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
145 150 155 160

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
 165 170 175

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
 180 185 190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
 195 200 205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
 210 215 220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225 230 235 240

Gln Tyr Glu Ile Val
 245

<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (60).. (794)

<400> 90

gcgtctcgct ctctgtgttc caatcgcccg gtgcggtggt gcagggctctc gggctagtc 59

atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt 107

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys

1 5 10 15

ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc 155

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20 25 30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35 40 45

tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc 251

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50 55 60

att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt 299

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65 70 75 80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85 90 95

ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395
 Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

100 105 110

gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag 443
 Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

115 120 125

gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta 491
 Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

130 135 140

gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga 539
 Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg

145 150 155 160

gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt 587
 Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser

165 170 175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta 635
 Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val

180 185 190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa 683
 Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu

195 200 205

atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg 731

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu

210

215

220

att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac 779

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn

225

230

235

240

cag tat gag ata gtg taaccaatg tatctgtggg cctattcctc tctaccttta 834

Gln Tyr Glu Ile Val

245

aggacattta gggcccccc tgtgaattag aaagttgctt ggctggagaa ctgacaacac 894

tacttactga tagacaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga 954

cctaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca 1014

atcaagatgt atgtttgcta tgttctaagt ccaccttcta tcccattcat gtagatcgt 1074

tgaaaccctg taccctctg aaacactgga agagctagta aattgtaaat gaagtaatac 1134

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gctattttga tgtagtgta caagatggaa aattgattcc tctgactttg ctattgatgt 1254

agtgtgatag aaaattcacc cctctgaact ggctccttcc cagtcaaggt tatctggttt 1314

gattgtataa ttgacacaa gaagttaaaa tgttttatga ctctctgttc tgctgacagg 1374

cagagagtca cattgtgtaa ttttaatttca gtcagtcaat agatggcatc cctcatcagg 1434

gttgccagat ggtgataaca gtgtaaggcc ttgggtctaa ggcatccacg actggaaggg 1494

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tttagctggt accagggtga tatgacttgt caatattatg gtcaacttta agtccttagtt 1734

ttcgtttgtg cctttgatta ataagtataa ctcttataca ataaatactg ctttcctct 1793

<210> 91

<211> 180

<212> PRT

<213> Homo sapiens

<400> 91

Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

1 5 10 15

Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu

20 25 30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala

315/735

35

40

45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

50

55

60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

65

70

75

80

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

85

90

95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

100

105

110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

115

120

125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

130

135

140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

145

150

155

160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser

165

170

175

Ala Leu Leu Gln

180

<210> 92

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26).. (565)

<400> 92

tttttcagct aaaggggaga tctgg atg gca tct act tcg tat gac tat tgc 52

Met Ala Ser Thr Ser Tyr Asp Tyr Cys

1

5

aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg 100

Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly

10

15

20

25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148

Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu

30

35

40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 196

Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu

45

50

55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 244

Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu

317/735

60

65

70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc 292

Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala

75

80

85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 340

Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu

90

95

100

105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 388

Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr

110

115

120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 436

Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu

125

130

135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac 484

Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr

140

145

150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg 532

Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu

155

160

165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585

Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln

170

175

180

318/735

acatcttgga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag 645
 ttctgagcgg gtcattggggc aacacgggta gcggggagag cacggggtag ccggagaagg 705
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 ttgaccagg gctgtctccc tccagagcct ccctccggac aatgagtcce ccctcttgtc 825
 tcccaccctg agattgggca tgggggtcgg tgtggggggc atgtgctgcc tgttggtatg 885
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 ctccctttga gggagagcac acctt 970

<210> 93

<211> 331

<212> PRT

<213> Homo sapiens

<400> 93

Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe

1

5

10

15

Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn

20

25

30

Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu

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35	40	45
Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala		
50	55	60
Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp		
65	70	75
		80
Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile		
	85	90
		95
Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly		
100	105	110
Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly		
115	120	125
Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr		
130	135	140
Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala		
145	150	155
		160
Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser		
	165	170
		175
Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu		
180	185	190

Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser
195 200 205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile
210 215 220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr
225 230 235 240

Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala
245 250 255

Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr
260 265 270

Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu
275 280 285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu
290 295 300

Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln
305 310 315 320

Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His
325 330

<211> 2039

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175).. (1167)

<400> 94

attatgcaga tgcacggctg gaggtgggat ccacacagct cagaacagct ggatcttgct 60

cacactcttt caagagaagc ttccttgggt taagaaaaaa aacgaaccct tccagtcagg 120

tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg 177

Met

1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225

Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg

5

10

15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273

Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu

20

25

30

gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321

Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala

35

40

45

gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369
Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile
50 55 60 65

ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa 465
Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu
85 90 95

acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc 561
Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile
115 120 125

ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg 657
Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val
150 155 160

Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala
165 170 175

gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag 753
Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys
180 185 190

gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt 801
Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu
195 200 205

ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt 849
Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg
210 215 220 225

gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg 897
Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp
230 235 240

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc 945
Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly
245 250 255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act 993
Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr
260 265 270

tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca 1041
Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser
324/735

275

280

285

aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg 1089

Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg

290

295

300

305

cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc 1137

Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile

310

315

320

tat cag cgt ctg aat cca tgc cat acc cac tgaccccaga ccagtgcagc 1187

Tyr Gln Arg Leu Asn Pro Cys His Thr His

325

330

cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga 1247

taaagagggc aaggtaaagt ttatggagct gagtgttagt gactttggca tttctgtagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat 1367

gctggagcct ggaataaggg aggagagggg actggagagt gtggggaata ggaagaagaa 1427

atttccttta gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc 1487

agcaatgaga aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac 1547

ttttggatac agcagaagaa acagcggctc cactaccgac ctgccccggg ttogatgtcc 1607

ttccaagaat gaagtctttc cctggtgatg gtcccctgcc ctgtctttcc agcatccact 1667

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ctgtcttgtc ctcttggaag tgtatctcag tcagccagtg gcttcttgat gatggcgggtg 1727

gaggtgggtgg ttgtagtgtg atggatcccc tttaggttat ttaggggtat atgtcccctg 1787

cttgaaccct gaaggccagg taatgagcca tggccattgt ccccagctga ggaccaggtg 1847

tctctaaaaa cccaaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907

ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967

gggaggccgg atctctagag ccatacctgct gagtgccctg tgtgtaagtc ctaataaact 2027

cacctactca cc 2039

<210> 95

<211> 407

<212> PRT

<213> Homo sapiens

<400> 95

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1 5 10 15

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20 25 30

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

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35

40

45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

50

55

60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65

70

75

80

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85

90

95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100

105

110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

115

120

125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130

135

140

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

145

150

155

160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

165

170

175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

180

185

190

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
195 200 205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
210 215 220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225 230 235 240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
245 250 255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
260 265 270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
275 280 285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
290 295 300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305 310 315 320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
325 330 335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
340 345 350

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Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
355 360 365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
370 375 380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
385 390 395 400

Val Cys Lys Tyr Lys Leu Leu
405

<210> 96

<211> 1409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (181)..(1401)

<400> 96

gctgtgcttg gcgcgtaccg tgcggtcct gtagttggag gacgggacgt cgcgcgccct 60

ttcccactag ccggagtagc ctctagttcg ttagtcaaaa cgtgaaaaaa aaagacctgc 120

tttgccctgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1 5 10 15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20 25 30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

35 40 45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

50 55 60

gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65 70 75 80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85 90 95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100 105 110

att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc	564
Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe	
115 120 125	
tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc	612
Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser	
130 135 140	
ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc	660
Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg	
145 150 155 160	
ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act	708
Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr	
165 170 175	
aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca	756
Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr	
180 185 190	
ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa	804
Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys	
195 200 205	
ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc	852
Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr	
210 215 220	
atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa	900

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225 230 235 240

gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga 948
Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
245 250 255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg 996
Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
260 265 270

cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac 1044
Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
275 280 285

ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc 1092
Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
290 295 300

aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta 1140
Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305 310 315 320

atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta 1188
Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
325 330 335

gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca 1236
Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
332/735

340	345	350	
aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca			1284
Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser			
355	360	365	
gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa			1332
Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu			
370	375	380	
aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt			1380
Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe			
385	390	395	400
gtg tgc aaa tat aaa cta tta taaaatcg			1409
Val Cys Lys Tyr Lys Leu Leu			
405			

<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

1	5	10	15
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Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

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	20		25		30
His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser					
	35		40		45
Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala					
	50		55		60
Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu					
	65		70		75
					80
Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His					
		85		90	95
Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys					
	100		105		110
Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu					
	115		120		125
Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val					
	130		135		140
Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser					
	145		150		155
					160
Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg					
		165		170	175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
195 200 205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
210 215 220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225 230 235 240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
245 250 255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
325 330 335

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Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
435 440 445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
450 455 460

Asp
465

<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477)..(1871)

<400> 98

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caccaaattct cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120

ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcc aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgac aaattgtgag aggaaaacag cctacccggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta tttcatcac ggtggaaaaat 420

tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

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Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
5 10 15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
20 25 30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
35 40 45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
50 55 60 65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
70 75 80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
85 90 95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
100 105 110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
338/735

115	120	125	
gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca			911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr			
130	135	140	145
aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca			959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr			
	150	155	160
gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa			1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln			
	165	170	175
aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa			1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu			
	180	185	190
gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg			1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu			
	195	200	205
agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa			1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu			
	210	215	220
ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc			1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala			
	230	235	240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247
 Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala

245 250 255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295
 Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

260 265 270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343
 Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser

275 280 285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391
 His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu

290 295 300 305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439
 Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu

310 315 320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487
 Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu

325 330 335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535
 Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val

340 345 350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583
 Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
 355 360 365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631
 Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
 370 375 380 385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679
 Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
 390 395 400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727
 Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
 405 410 415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775
 Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
 420 425 430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823
 Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
 435 440 445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871
 Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
 450 455 460 465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931
 341/735

taagggcag

1940

<210> 99

<211> 465

<212> PRT

<213> Homo sapiens

<400> 99

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

1 5 10 15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

20 25 30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser

35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala

50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu

65 70 75 80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His

85 90 95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys

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100	105	110
Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu		
115	120	125
Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val		
130	135	140
Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser		
145	150	155 160
Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg		
165	170	175
Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu		
180	185	190
Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr		
195	200	205
Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn		
210	215	220
Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser		
225	230	235 240
Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp		
245	250	255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
325 330 335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
405 410 415

344/735

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
435 440 445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
450 455 460

Asp
465

<210> 100

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477)..(1871)

<400> 100

gttaacttcc tgaccagga agtggcagca acagagggga ctagcagcga atatacttta 60

caccaaattc cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120

ccttggaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcc aaggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgata aaattgtgag aggaaaacag cctacccggt cctcttttct 300

tcaatacaaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

5

10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

20

25

30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

35

40

45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

50

55

60

65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719
 Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
 70 75 80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767
 Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
 85 90 95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815
 Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
 100 105 110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863
 Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
 115 120 125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca 911
 Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr
 130 135 140 145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959
 Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr
 150 155 160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007
 Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln
 165 170 175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055
 347/735

Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
180 185 190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
195 200 205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
210 215 220 225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
230 235 240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
245 250 255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
260 265 270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
275 280 285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu

290	295	300	305	
att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag				1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu				
	310	315	320	
aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg				1487
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu				
	325	330	335	
ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt				1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val				
	340	345	350	
ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag				1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln				
	355	360	365	
agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc				1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu				
370	375	380	385	
agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act				1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr				
	390	395	400	
tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac				1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp				
	405	410	415	
				349/735

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

435

440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

450

455

460

465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag

1940

<210> 101

<211> 685

<212> PRT

<213> Homo sapiens

<400> 101

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys

1

5

10

15

Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys

20

25

30

350/735

Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
35 40 45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
50 55 60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
65 70 75 80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
85 90 95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
100 105 110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
115 120 125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
130 135 140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
145 150 155 160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
165 170 175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
351/735

	180		185		190
Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu					
	195		200		205
Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe					
	210		215		220
Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile					
225		230		235	240
Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly					
	245		250		255
His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr					
	260		265		270
Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr					
	275		280		285
Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu					
	290		295		300
Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu					
305		310		315	320
Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln					
	325		330		335

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
340 345 350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
355 360 365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr
370 375 380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
385 390 395 400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr
405 410 415

Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr
420 425 430

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
435 440 445

Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
450 455 460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
465 470 475 480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
485 490 495

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
500 505 510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
515 520 525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val
530 535 540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
545 550 555 560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
565 570 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
580 585 590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
595 600 605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
610 615 620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625 630 635 640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
354/735

	645	650	655
Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg			
	660	665	670

Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
675 680 685

<210> 102

<211> 2783

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (128)..(2182)

<400> 102

gcacaagtgg accggggtgt tgggtgctag tcggcaccag aggcaagggt gcgaggacca 60

cggccggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtgc ggggcggcaa 120

ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser

1

5

10

acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217

Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser

355/735

15	20	25	30	
aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag	265			
Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln				
35	40	45		
tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat	313			
Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His				
50	55	60		
tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act	361			
Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr				
65	70	75		
ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca	409			
Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala				
80	85	90		
aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca	457			
Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala				
95	100	105	110	
aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag	505			
Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys				
115	120	125		
att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta	553			
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val				
130	135	140		
356/735				

gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc 601

Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu

145

150

155

ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga 649

Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg

160

165

170

aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg 697

Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val

175

180

185

190

tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc 745

Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu

195

200

205

aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg 793

Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly

210

215

220

gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga 841

Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg

225

230

235

acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa 889

Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys

240

245

250

caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg 937
 Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met
 255 260 265 270

tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa 985
 Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys
 275 280 285

gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca 1033
 Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser
 290 295 300

ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac 1081
 Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn
 305 310 315

cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt 1129
 Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe
 320 325 330

ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca 1177
 Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr
 335 340 345 350

gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa 1225
 Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys
 355 360 365

gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att 1273
 358/735

Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile

370

375

380

gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt 1321

Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu

385

390

395

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac 1369

Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His

400

405

410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct 1417

Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser

415

420

425

430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg 1465

Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg

435

440

445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc 1513

Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys

450

455

460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt 1561

Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val

465

470

475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa 1609

Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys

359/735

480	485	490	
gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac			1657
Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr			
495	500	505	510
tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt			1705
Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly			
	515	520	525
gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa			1753
Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys			
	530	535	540
aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca			1801
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala			
	545	550	555
aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac			1849
Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr			
	560	565	570
ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct			1897
Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro			
575	580	585	590
agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta			1945
Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu			
	595	600	605

aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag 1993
 Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln

610 615 620

gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat 2041
 Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn

625 630 635

gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act 2089
 Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr

640 645 650

ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa 2137
 Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys

655 660 665 670

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac 2182
 Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn

675 680 685

tgaaagactt ttcgaatgga ccctatggga ctctctttt ccactgtgag atctacaggg 2242

aacccaaaag aatgatctag agtatgttga agaagatgga catgtggtgg tacgaaaaca 2302

attcccctgt ggcctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362

actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttaaaa 2422

ggtttttcag acaattttgc agaaaggtgc attgattcctt aaattctctc tgttgagagc 2482

atttcagcca gaggactttg gaactgtgaa tatacttcct gaaggggagg gagaaggag 2542

gaagctccca tgttgtttta aggctgtaat tggagcagct tttggctgcg taactgtgaa 2602

ctatggccat atataatttt ttttcattaa ttttgaaga tacttgtggc tggaaaagtg 2662

cattccttgt taataaactt tttatttatt acageccaaa gagcagtatt tattatcaaa 2722

atgtcttttt ttttatgttg accattttta accgttggca ataaagagta tgaaaacgca 2782

g 2783

<210> 103

<211> 161

<212> PRT

<213> Homo sapiens

<400> 103

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala

1 5 10 15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr

20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val

35 40 45

362/735

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys
85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
115 120 125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
130 135 140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145 150 155 160

Leu

<210> 104

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 104

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ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15

20

25

30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35

40

45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

50

55

60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

65

70

75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg 351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met
80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
Lys Arg Leu
160

aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tgggtggtctc 652

acctctccag ggggccccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgcccaga gctcggtga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaattttt 1132

tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcctt tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct ttggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaca gagatggggt cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcaatt 1589

<210> 105

<211> 161

<212> PRT

<213> Homo sapiens

<400> 105

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala

1 5 10 15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr

20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val

35 40 45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln

50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr

65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys

85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly

100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile

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115

120

125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val

130

135

140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg

145

150

155

160

Leu

<210> 106

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (552)

<400> 106

ccttttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

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Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
 15 20 25 30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207
 Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
 35 40 45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255
 Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
 50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303
 Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
 65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351
 Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met
 80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
 Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
 95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
 Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
 115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
 Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
 369/735

130

135

140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543

Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145

150

155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592

Lys Arg Leu

160

aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tgggtggtctc 652

acctctccag ggggccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaatttt 1132

tttttaaata caaggagggg gctattaaca ccagtacag acatatccac aaggtcgtaa 1192

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atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252
 tgccagatct tcagtgcgcc tttccataca gggatTTTT tctcatagag taattatatg 1312
 aacagtTTTT atgacctcct ttTggtctga aatactttcg aacagaattt ctttttttta 1372
 aaaaaaaaca gagatggggT ctTactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432
 aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492
 tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552
 tggtgtcatt ttcccatTTg ccaatgtagt ctcaatt 1589

<210> 107

<211> 249

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val

1 5 10 15

Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val

20 25 30

Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys

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35	40	45
Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn		
50	55	60
Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu		
65	70	75 80
Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met		
85	90	95
Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val		
100	105	110
Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys		
115	120	125
Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro		
130	135	140
Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro		
145	150	155 160
Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met		
165	170	175
Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu		
180	185	190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His
195 200 205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val
210 215 220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile
225 230 235 240

Gly Phe Phe Leu Gly Lys Phe Ile Leu
245

<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232).. (978)

<400> 108

agtgcgcgtg gccgtggcgg ctggtgtggg gttgagtcag ttgtgggacc cggagctgct 60

gacccagcgg gtggcccacc gaaccggtga cacagcggca ggcgttaggg ctcgggagcc 120

gcgagccttg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgcccc 180

agtcagcaaa ccgccgccgc gggcgcgccc ccgctctgcg ctgtctctcc g atg gcg 237

Met Ala

1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat 285

Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp

5

10

15

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333

Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr

20

25

30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381

Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys

35

40

45

50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429

Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly

55

60

65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477

Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro

70

75

80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln

85

90

95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573

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Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys

100

105

110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt 621

Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe

115

120

125

130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa 669

Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys

135

140

145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca 717

Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro

150

155

160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag 765

His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu

165

170

175

tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg 813

Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg

180

185

190

cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat 861

His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp

195

200

205

210

aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt 909

Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser

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215

220

225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957

Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe

230

235

240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttctt 1008

Phe Leu Gly Lys Phe Ile Leu

245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcat tggtagtatg 1068

gcccacggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacggtta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308

tggtatttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368

atttagattg ctaatccac tcattcagga aatgccaaga ggtattcctt ggggaaatgg 1428

tgcctcttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tgttgactga gtttttcac cttacaatcc tgtcccatgg 1548

tatttaacat aaaaaaaaaat aaaactgtta acagattcctt gctcgat 1595

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<210> 109

<211> 540

<212> PRT

<213> Homo sapiens

<400> 109

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

1 5 10 15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20 25 30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro

100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260 265 270

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Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg
405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
379/735

420	425	430
Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg		
435	440	445
Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu		
450	455	460
Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp		
465	470	475 480
Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val		
485	490	495
Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly		
500	505	510
Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly		
515	520	525
Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu		
530	535	540

<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 110

aaccgtaaca gccaccagac aagcttcagt ggccggccct tcacatccag acttgccctga 60

gaggacccac ctctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

1

5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

15

20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

60

65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

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70	75	80	85	
ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa				404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu				
	90	95	100	
gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg				452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu				
	105	110	115	
ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca				500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro				
	120	125	130	
ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag				548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln				
	135	140	145	
cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat				596
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp				
150	155	160	165	
ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc				644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys				
	170	175	180	
ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag				692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln				
	185	190	195	

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg	740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu	
200 205 210	
 gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc	788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg	
215 220 225	
 cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt	836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys	
230 235 240 245	
 gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg	884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg	
250 255 260	
 cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca	932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro	
265 270 275	
 cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg	980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser	
280 285 290	
 ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc	1028
Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile	
295 300 305	

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076
 Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
 310 315 320 325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124
 Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
 330 335 340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172
 Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
 345 350 355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220
 Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
 360 365 370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268
 Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser
 375 380 385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316
 Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr
 390 395 400 405

gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc 1364
 Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu
 410 415 420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412
 384/735

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425

430

435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440

445

450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455

460

465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470

475

480

485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490

495

500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

505

510

515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111

<211> 540

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

1

5

10

15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20

25

30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35

40

45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50

55

60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65

70

75

80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85

90

95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260 265 270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
388/735

405

410

415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu

420

425

430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg

435

440

445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu

450

455

460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp

465

470

475

480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val

485

490

495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

500

505

510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

515

520

525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

530

535

540

<210> 112

<211> 1810

389/735

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 112

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gaggaccacac ctctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

1

5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

15

20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

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65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct	356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro	
70 75 80 85	
ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa	404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu	
90 95 100	
gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg	452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu	
105 110 115	
ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca	500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro	
120 125 130	
ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag	548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln	
135 140 145	
cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat	596
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp	
150 155 160 165	
ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc	644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys	
170 175 180	

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692
 Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185

190

195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740
 Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu

200

205

210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788
 Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg

215

220

225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836
 Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys

230

235

240

245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884
 Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg

250

255

260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932
 Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

265

270

275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980
 His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser

280

285

290

ggg ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028

Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
 295 300 305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076
 Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
 310 315 320 325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124
 Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
 330 335 340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172
 Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
 345 350 355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220
 Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
 360 365 370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268
 Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser
 375 380 385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316
 Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr
 390 395 400 405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc 1364
 Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu
 393/735

410	415	420	
atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat			1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His			
425	430	435	
att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca			1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro			
440	445	450	
ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc			1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile			
455	460	465	
aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc			1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu			
470	475	480	485
tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc			1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile			
490	495	500	
aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc			1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala			
505	510	515	
aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc			1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser			
520	525	530	

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 113

<211> 382

<212> PRT

<213> Homo sapiens

<400> 113

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe

20

25

30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35

40

45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

50

55

60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu

65

70

75

80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
115 120 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
290 295 300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
370 375 380

<210> 114

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201).. (1346)

<400> 114

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aacagcagcg gagtttttaa ctttaaatac acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

5

10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

20

25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

30

35

40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

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Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
45 50 55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
60 65 70 75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
80 85 90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
95 100 105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
110 115 120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
125 130 135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
140 145 150 155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu
399/735

160

165

170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761

Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys

175

180

185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809

Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro

190

195

200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857

Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val

205

210

215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905

Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly

220

225

230

235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953

Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser

240

245

250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001

Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr

255

260

265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049

Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro

270

275

280

400/735

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097
 Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

285

290

295

aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca 1145
 Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala

300

305

310

315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193
 Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

320

325

330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241
 Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

335

340

345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289
 Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

350

355

360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
 Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

365

370

375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386
 Leu Glu Ile

380

ggagaagaaa aaaggtgctg tagaaagtc accaggtgtt aattttgatc cggtaggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcactggggg tgtatggggt agatgggtgg agaggaggag gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatatt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcacttigaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggtg 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046

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gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406

atactgggtt tgtaattat gattctttat tttctctcct ttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaatttttagt actgtaaaca ggcttttagtc attaatgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaaatgt gcctaaatga attttgcagt aactgggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttattt ggaatgcaag agaggttgaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcat gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttggt tgacattcca tgttaaacta cggtcatggt cagcttcatt gcatgtaatg 3006

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3074

<210> 115

<211> 382

<212> PRT

<213> Homo sapiens

<400> 115

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
20 25 30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
35 40 45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
50 55 60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
404/735

115	120	125
Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys		
130	135	140
Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu		
145	150	155 160
Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile		
165	170	175
Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys		
180	185	190
Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile		
195	200	205
Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn		
210	215	220
Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val		
225	230	235 240
Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro		
245	250	255
Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser		
260	265	270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
290 295 300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
370 375 380

<210> 116

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201).. (1346)

<400> 116

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aacagcagcg gagttttaaa ctttaaatac acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

5

10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

20

25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

30

35

40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

45

50

55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

60

65

70

75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473
 Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
 80 85 90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521
 Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
 95 100 105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569
 Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
 110 115 120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617
 Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
 125 130 135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665
 Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
 140 145 150 155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713
 Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu
 160 165 170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761
 Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys
 175 180 185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809
 408/735

Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro

190

195

200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857

Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val

205

210

215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905

Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly

220

225

230

235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953

Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser

240

245

250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001

Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr

255

260

265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049

Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro

270

275

280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097

Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

285

290

295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca 1145

Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala

409/735

300	305	310	315	
gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat				1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His				
	320	325	330	
gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta				1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu				
	335	340	345	
gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct				1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro				
	350	355	360	
tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac				1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp				
	365	370	375	
ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt				1386
Leu Glu Ile				
380				
ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgatc cgggtggaggt				1446
ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt				1506
tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg				1566
gtattttaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata				1626

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggta 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046

ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcttaata tttacaacac 2166

acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

tataaactca caaacacaga ttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286

tctcatggat ttttgtgggtg tgggccaata tgggtgtttac attatataat tcctgctgtg 2346

gcaagtaaag cacacttttt ttttctcta aaatgttttt ccctgtgtat cctattatgg 2406

atactggttt tgttaattat gattctttat tttctctcct ttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaatttttagt actgtaaaca ggcttttagtc attaatgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaaatgt gcctaaatga attttgcagt aactgggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagttagc agtcttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttatth ggaatgcaag agaggttgaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcat gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttggt tgacattcca tgttaaacta cggatcatgtt cagcttcatt gcatgtaatg 3006

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tttagtat 3074

<210> 117

<211> 398

<212> PRT

<213> Homo sapiens

<400> 117

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
1 5 10 15

Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala
20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg.
100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
165 170 175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
180 185 190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
195 200 205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
210 215 220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225 230 235 240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
245 250 255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
260 265 270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
275 280 285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
290 295 300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
414/735

305 310 315 320

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
340 345 350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
355 360 365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
370 375 380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
385 390 395

<210> 118

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1269)

<400> 118

cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttggagg 60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
 Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
 110 115 120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
 Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
 125 130 135 140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
 Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
 145 150 155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
 Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
 160 165 170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639
 Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
 175 180 185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687
 Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
 190 195 200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735
 Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
 205 210 215 220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783
 417/735

Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
225 230 235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
240 245 250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
255 260 265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
270 275 280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
285 290 295 300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu
305 310 315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
320 325 330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp

335

340

345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167

Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350

355

360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215

Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

365

370

375

380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263

Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385

390

395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319

Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagaccca gcccaggtt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatgt cccctgccct gtctttccag catccactct 1679

cccttgtcct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tccccctccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtcccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcac 2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

1 5 10 15

Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala

20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35 40 45

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Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
165 170 175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
180 185 190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
421/735

195	200	205
Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr		
210	215	220
Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala		
225	230	235 240
His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu		
245	250	255
Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr		
260	265	270
Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg		
275	280	285
Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro		
290	295	300
Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg		
305	310	315 320
Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr		
325	330	335
Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu		
340	345	350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
 355 360 365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
 370 375 380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
 385 390 395

<210> 120

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1269)

<400> 120

cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttgagg 60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu

15

20

25

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gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207
 Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255
 Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303
 Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351
 Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399
 Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
 Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
 Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
 Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
 145 150 155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
 Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
 160 165 170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639
 Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
 175 180 185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687
 Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
 190 195 200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735
 Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
 205 210 215 220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783
 Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
 225 230 235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831
 Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
 240 245 250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879
 425/735

Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu

255

260

265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927

Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg

270

275

280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975

Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser

285

290

295

300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023

Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu

305

310

315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071

Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly

320

325

330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119

Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp

335

340

345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167

Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350

355

360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215

Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

426/735

365	370	375	380
-----	-----	-----	-----

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385	390	395
-----	-----	-----

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319
Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agccaagag ttagaacagt 1559

tggtacagg agaagaaaca gcggtccac tacagacca gcccaggtt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatgg cccctgccct gtctttccag catccactct 1679

cccttgtcct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg 1739

ggtggttgct atgtgatggg tcccctccag gttactaaag ggtgcatgct ccctgcttga 1799

aactgaagg gcagggtgtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt ctgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatac 2054

<210> 121

<211> 108

<212> PRT

<213> Homo sapiens

<400> 121

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe

1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu

20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val

50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp

65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala

428/735

85

90

95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu

100

105

<210> 122

<211> 1546

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89).. (412)

<400> 122

actaggcaga gccgtggaac cgccgccagg tcgctgttgg tccacgccgc ccgtcgcgcc 60

gcccgcgccgc tcagcgtccg ccgccgcc atg gga gtg cag gtg gaa acc atc 112

Met Gly Val Gln Val Glu Thr Ile

1

5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg 160

Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val

10

15

20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc 208

Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser

25

30

35

40

429/735

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256
 Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val

45

50

55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304
 Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg

60

65

70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352
 Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His

75

80

85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400
 Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu

90

95

100

cta aaa ctg gaa tgacaggaat ggcctcctcc cttagctccc tggtcttgga 452
 Leu Lys Leu Glu

105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgctt ccgacacctc tgtttctct tcccccttct cctcgtatgt gtgtttacct 632

aaactatatg ccataaacct caagttactc attttatattt gttttcattt tgggggtgaag 692



attcagtttc agtcttttgg atataggttt ccaattaagt acatggtcaa gtattaacag 752

cacaagtggg aggttaacat tagaatagga attggtgttg gggggggggg ttgcaagaat 812

attttatttt aattttttgg atgaaatttt tatctattat atattaaaca ttcttgctgc 872

tgcgctgcaa agccatagca gatttgaggc gctgttgagg actgaattac tctccaagtt 932

gagagatgtc tttgggttaa attaaaagcc ctacctaaaa ctgaggtggg gatggggaga 992

gcctttgcct ccaccattcc caccaccct ccccttaaac cctctgcctt tgaaagtaga 1052

tcattgtcac tgcaatgctg gacactacag gtatctgtcc ctgggccagc aggacctct 1112

gaagccttct ttgtggcctt tttttttttt tcctcctgtg gtttttctaa tggactttca 1172

ggaattttgt aatctcataa cttccaagc tccaccactt cctaaatctt aagaacttta 1232

attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtga agccagcca 1292

tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggatcatgc agcttcagca 1352

tctcctgttt ttgatgctt ggctccctct gctgatctca gtttcctggc ttttcctccc 1412

tcagccccct ctcacccctt tgctgtcctg tgtagtgatt tggtagagaa tcgttgctgc 1472

acccttcccc cagcaccatt tatgagtctc aagttttatt attgcaataa aagtgttta 1532

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1546

<210> 123

<211> 679

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly
1 5 10 15

Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala
20 25 30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe
35 40 45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile
50 55 60

Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys
65 70 75 80

Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn
85 90 95

Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly
100 105 110

Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser
115 120 125

Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala
130 135 140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met
145 150 155 160

Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu
165 170 175

Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro
180 185 190

Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile
195 200 205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
210 215 220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val
225 230 235 240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
245 250 255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
260 265 270

Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser
275 280 285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala
290 295 300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys
305 310 315 320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val
325 330 335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val
340 345 350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn
355 360 365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp
370 375 380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val
385 390 395 400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn
405 410 415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser
434/735

	420	425	430
Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu			
435	440	445	
Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr			
450	455	460	
Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile			
465	470	475	480
Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser			
485	490	495	
Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser			
500	505	510	
Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe			
515	520	525	
Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala			
530	535	540	
Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr			
545	550	555	560
Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu			
565	570	575	

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
580 585 590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
595 600 605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His
610 615 620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
625 630 635 640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
645 650 655

Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
660 665 670

Arg Tyr Val Ile Leu Arg Met
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<211> 2916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81).. (2117)

<400> 124

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aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala

1

5

10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161

Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu

15

20

25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209

Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp

30

35

40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257

Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu

45

50

55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305

Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val

60

65

70

75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353

Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp

80

85

90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc 401
Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val

95

100

105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg 449
Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu

110

115

120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497
Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly

125

130

135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545
Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu

140

145

150

155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593
Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile

160

165

170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag 641
Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys

175

180

185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc 689
Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala

190

195

200

tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg 737

438/735

Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro
 205 210 215

ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg 785
 Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser
 220 225 230 235

gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt 833
 Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys
 240 245 250

ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct 881
 Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser
 255 260 265

gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa 929
 Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu
 270 275 280

gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct 977
 Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser
 285 290 295

gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga 1025
 Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg
 300 305 310 315

aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag 1073
 Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu

320	325	330	
agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc			1121
Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr			
335	340	345	
gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt			1169
Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser			
350	355	360	
caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac			1217
Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His			
365	370	375	
acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta			1265
Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu			
380	385	390	395
cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc			1313
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro			
400	405	410	
tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc			1361
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly			
415	420	425	
atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa			1409
Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu			
430	435	440	

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att		1457
Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile		
445	450	455
cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac		1505
Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His		
460	465	470 475
tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt		1553
Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly		
480	485	490
gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat		1601
Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp		
495	500	505
aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc		1649
Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala		
510	515	520
tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att		1697
Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile		
525	530	535
ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct		1745
Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser		
540	545	550 555

tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt	1793
Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly	
560 565 570	

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg	1841
Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met	
575 580 585	

ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa	1889
Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu	
590 595 600	

ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc	1937
Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro	
605 610 615	

atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg	1985
Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp	
620 625 630 635	

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt	2033
Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe	
640 645 650	

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc	2081
Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala	
655 660 665	

atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt	2127
442/735	

Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met

670

675

tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga 2187

atgattacag tgtaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg 2247

aagtgttact tgtgctataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgagggtcc ctttcccttc tgggctgtga 2367

attcctgtac atatttctct actttttgta tcaggcttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttat 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847

ttaaattggga cagccttcca tggtcatttg tctacctctt aactgaataa aaaagcctac 2907

<210> 125

<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala

1 5 10 15

Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

20 25 30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35 40 45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu

50 55 60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro

65 70 75 80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp

85 90 95

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln

100 105 110

444/735

Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
115 120 125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
130 135 140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145 150 155 160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
165 170 175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
180 185 190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu
195 200 205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
210 215 220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
225 230 235 240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
245 250 255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
445/735

260

265

270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met

275

280

285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81).. (944)

<400> 126

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acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln

1

5

10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161

Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln

15

20

25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209

Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr

30

35

40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257

Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val

45

50

55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305

Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala

60

65

70

75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag 353

Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln

80

85

90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac 401

Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr

95

100

105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc 449

Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg

110

115

120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt 497

Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly

125

130

135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg 545

Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu

140

145

150

155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593
 Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn
 160 165 170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641
 Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn
 175 180 185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689
 Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala
 190 195 200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737
 Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu
 205 210 215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785
 Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly
 220 225 230 235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833
 Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu
 240 245 250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881
 Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu
 255 260 265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929
 448/735

Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val

270

275

280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984

Gly Leu Tyr Ala Met

285

ccggtggaag gccttctttc tagagaggga attctcttgg ctggcttcct taccgtgggc 1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagcctatg gcattctccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acaccctaag gtggcagctg tctcaaact ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344

atgttggtgc ttgtgttttt gtcttatttt tgttgagacc actctgttcc tggctcagcc 1404

tcaaatgcag tatttttggg gtgttctgtt gtttttatag cagggttggg gtgggtttttg 1464

agccatgcgt ggggtggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524

tgtgaaataa taaacaacat tgtctg

1550

<210> 127

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1

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15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

20

25

30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

35

40

45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

50

55

60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

65

70

75

80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

85

90

95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

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115

120

125

Ile Lys Cys Val Ala Phe Asp

130

135

<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(454)

<400> 128

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Met Ala Cys

1

ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106

Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg

5

10

15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154

Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu

20

25

30

35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202

Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn

40

45

50

451/735

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg 250
 Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly

55

60

65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298
 Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly

70

75

80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346
 Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val

85

90

95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394
 Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
 100 105 110 115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442
 Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys

120

125

130

gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494
 Val Ala Phe Asp

135

ctctgctccc ctg

507

<210> 129

452/735

<211> 662

<212> PRT

<213> Homo sapiens

<400> 129

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn

1 5 10 15

Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn

20 25 30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp

35 40 45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys

50 55 60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser

65 70 75 80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr

85 90 95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu

100 105 110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys

115 120 125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
130 135 140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
145 150 155 160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro
165 170 175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
180 185 190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
195 200 205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
210 215 220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
225 230 235 240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu
245 250 255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr
260 265 270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln
275 280 285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys
290 295 300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val
305 310 315 320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala
325 330 335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe
340 345 350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp
355 360 365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln
370 375 380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp
385 390 395 400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu
405 410 415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe
420 425 430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn
455/735

435	440	445
Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile		
450	455	460
Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp		
465	470	475
Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu		
	485	490
Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser		
500	505	510
Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr		
515	520	525
Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn		
530	535	540
Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly		
545	550	555
Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln		
	565	570
Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln		
580	585	590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn
595 600 605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe
610 615 620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn
625 630 635 640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg
645 650 655

Leu Arg Ile Ser Glu Lys
660

<210> 130

<211> 2251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(2059)

<400> 130

cttggctgga cagtttgtga aactgtgttg ccgggcaact ggacatcctt ttgttcaata 60

tcagtgggttc aaa atg aat aaa gag att cca aat gga aat aca tca gag 109

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu

1

5

10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157

Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys

15

20

25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg 205

Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu

30

35

40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc 253

Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val

45

50

55

60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg 301

Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu

65

70

75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct 349

Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro

80

85

90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag 397

Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu

95

100

105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga 445

Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly

458/735

110	115	120	
acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag			493
Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys			
125	130	135	140
aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act			541
Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr			
	145	150	155
gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca			589
Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr			
	160	165	170
act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat			637
Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn			
	175	180	185
atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg			685
Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val			
	190	195	200
tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca			733
Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser			
205	210	215	220
ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt			781
Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe			
	225	230	235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829
 Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly

240

245

250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877
 His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala

255

260

265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925
 Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu

270

275

280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973
 Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp
 285 290 295 300

atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021
 Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp

305

310

315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069
 Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln

320

325

330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117
 Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile

335

340

345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165
Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr
350 355 360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213
Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr
365 370 375 380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261
Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg
385 390 395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309
Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu
400 405 410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357
Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met
415 420 425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405
Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala
430 435 440

gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453
Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro
445 450 455 460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501
461/735

Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp
465 470 475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549
Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr
480 485 490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597
Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr
495 500 505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645
Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val
510 515 520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693
Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys
525 530 535 540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741
Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His
545 550 555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789
Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn
560 565 570

ggc cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837
Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr
462/735

575	580	585	
cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt			1885
His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly			
590	595	600	
aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act			1933
Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr			
605	610	615	620
cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt			1981
Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe			
	625	630	635
agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt			2029
Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser			
	640	645	650
ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa			2079
Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys			
655	660		
gtagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt			2139
gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc			2199
aggactttga gatgttgaaa ttacattatt taattacaga cttcctcttt ct			2251

<210> 131

<211> 824

<212> PRT

<213> Homo sapiens

<400> 131

Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala

1

5

10

15

Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg

20

25

30

Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala

35

40

45

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg

50

55

60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys

65

70

75

80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met

85

90

95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala

100

105

110

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys

115

120

125

464/735

Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val

130

135

140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp

145

150

155

160

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile

165

170

175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val

180

185

190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val

195

200

205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu

210

215

220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro

225

230

235

240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro

245

250

255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys

260

265

270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr

465/735

275	280	285
Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val		
290	295	300
Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp		
305	310	315 320
Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp		
325	330	335
Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn		
340	345	350
Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu		
355	360	365
Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu		
370	375	380
Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu		
385	390	395 400
Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly		
405	410	415
Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn		
420	425	430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
435 440 445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
450 455 460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
465 470 475 480

Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
485 490 495

Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
500 505 510

Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
515 520 525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
530 535 540

Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545 550 555 560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
565 570 575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
580 585 590

467/735

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
595 600 605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
610 615 620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
625 630 635 640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
645 650 655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
660 665 670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
675 680 685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
690 695 700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705 710 715 720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
725 730 735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
468/735

740

745

750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro

755

760

765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp

770

775

780

Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg

785

790

795

800

Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser

805

810

815

Asp Arg Leu Arg Ile Ser Glu Lys

820

<210> 132

<211> 2828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (165).. (2636)

<400> 132

ggggcgggga gcggaacttcc tcctctgagg gccgtgccgc gctgccagat ttgttcttcc 60

469/735

gcccctgcct ccgcggctcg gaggcgagcg gaaggtgccc cggggccgag gcccgtgacg 120

gggcggggcgg gagccccggc agtccgggggt cgccggcgag ggcc atg tcg ctg ttg 176

Met Ser Leu Leu

1

ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg 224

Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro

5

10

15

20

ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg 272

Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro

25

30

35

ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc cgg 320

Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg

40

45

50

ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc 368

Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg

55

60

65

ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct 416

Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro

70

75

80

gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt 464

Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly

470/735

85	90	95	100	
tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act				512
Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr				
	105	110	115	
gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac				560
Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn				
	120	125	130	
cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc				608
Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys				
	135	140	145	
cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat				656
Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn				
	150	155	160	
aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg				704
Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val				
165	170	175	180	
cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc				752
His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe				
	185	190	195	
acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca				800
Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro				
	200	205	210	

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa 848
 Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln

215

220

225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg 896
 Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu

230

235

240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg 944
 Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp

245

250

255

260

ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg 992
 Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met

265

270

275

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta 1040
 Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val

280

285

290

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata 1088
 Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile

295

300

305

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat 1136
 Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn

310

315

320

```

ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg      1184
Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala
325              330              335              340

aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac      1232
Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His
              345              350              355

ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta      1280
Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu
              360              365              370

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa      1328
Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu
              375              380              385

tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag      1376
Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys
              390              395              400

gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt      1424
Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe
405              410              415              420

ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct      1472
Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser
              425              430              435

gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa      1520

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473/735

Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys

440

445

450

gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat 1568

Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn

455

460

465

gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc 1616

Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala

470

475

480

aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa 1664

Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu

485

490

495

500

atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa 1712

Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys

505

510

515

gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt 1760

Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val

520

525

530

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta 1808

Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu

535

540

545

gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata 1856

Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile

474/735

550	555	560	
cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg	1904		
Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp			
565	570	575	580
gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt	1952		
Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys			
585	590	595	
ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg	2000		
Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met			
600	605	610	
atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt	2048		
Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys			
615	620	625	
gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa	2096		
Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys			
630	635	640	
gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca	2144		
Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser			
645	650	655	660
aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa	2192		
Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln			
665	670	675	

aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac 2240
 Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr

680

685

690

tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg 2288
 Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly

695

700

705

aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag 2336
 Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys

710

715

720

act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct 2384
 Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser
 725 730 735 740

gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca 2432
 Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro

745

750

755

ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca 2480
 Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr

760

765

770

cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca 2528
 Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser

775

780

785

agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca 2576
 Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro
 790 795 800

gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga 2624
 Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg
 805 810 815 820

att tct gaa aaa tgacctcctt gtttttgaaa gttagcataa ttttagatgc 2676
 Ile Ser Glu Lys

ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

gtagagaaaag aatagtagta actgtttcat agcaaacttc aggactttga gatgttgaaa 2796

ttacattatt taattacaga cttcctcttt ct 2828

<210> 133

<211> 919

<212> PRT

<213> Homo sapiens

<400> 133

Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn Glu Thr

1 5 10 15

Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser

20 25 30

477/735

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys
35 40 45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp
50 55 60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys
65 70 75 80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu
85 90 95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile
100 105 110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu
115 120 125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu
130 135 140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr
145 150 155 160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe
165 170 175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr
478/735

	180	185	190
Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly			
	195	200	205
Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg			
	210	215	220
Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu			
	225	230	235 240
Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr			
	245	250	255
Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr			
	260	265	270
Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly			
	275	280	285
Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala			
	290	295	300
Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu			
	305	310	315 320
Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro			
	325	330	335

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr
340 345 350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser
355 360 365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly
370 375 380

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala
385 390 395 400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile
405 410 415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala
420 425 430

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg
435 440 445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
450 455 460

Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys
465 470 475 480

Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys
485 490 495

480/735

Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln
500 505 510

Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala
515 520 525

Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile
530 535 540

Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile
545 550 555 560

Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr
565 570 575

Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln
580 585 590

Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser
595 600 605

Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His
610 615 620

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala
625 630 635 640

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp
481/735

	645	650	655
Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala			
	660	665	670
Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala			
	675	680	685
Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg			
	690	695	700
Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala			
705	710	715	720
Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp			
	725	730	735
Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu			
	740	745	750
Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp			
	755	760	765
Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile			
	770	775	780
Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp			
785	790	795	800

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val
805 810 815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser
820 825 830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val
835 840 845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu
850 855 860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe
865 870 875 880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys
885 890 895

Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr
900 905 910

Ser Ser Ser Phe Leu Glu Val
915

<210> 134

<211> 3612

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (427).. (3183)

<400> 134

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cctccccgcc cgccctctct cctcccttc ctcctcccg ctgcttctt ctcacgccgg 120

gagcaggctc ccgcctcgca ccgtgcccc gcgagcagct cctcttctcc cgaggcgcg 180

ggggcgcccc cgcgagcccc gcggctgaga cccgcagcc tggaggaggg ctgtccgggg 240

ctttggatgc tgctgctagg ggtggtggga gcagccgtgg gacgcgtggc cgggagcggg 300

ggtgacagcc tgggattccg ggggcttctc ttccttgtec tcctcctctc ctctctattc 360

ccagtgtggc cgtggctgac actaaagact ttgtagccat caacccgagt gcagtttcga 420

tggaaa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat 468

Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn

1

5

10

gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca 516

Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro

15

20

25

30

gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta 564

Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu

35

40

45

aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat ggc tgg aat gag 612

Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu

50

55

60

ttt gat att agt gaa gat gag cca ctg tgg aag aag tat att tct cag 660

Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln

65

70

75

ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt 708

Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser

80

85

90

gtt tta atg cat cag ttt gat gat gcc gtc agt atc act gtg gca ata 756

Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile

95

100

105

110

ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa 804

Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys

115

120

125

tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg 852

Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val

130

135

140

cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt 900

Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly

485/735

145	150	155	
gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc			948
Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg			
160	165	170	
ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt			996
Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly			
175	180	185	190
gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act			1044
Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr			
	195	200	205
aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg			1092
Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu			
210	215	220	
gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat			1140
Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn			
225	230	235	
tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca			1188
Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro			
240	245	250	
aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc			1236
Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser			
255	260	265	270

ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta 1284
Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu

275

280

285

ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct 1332
Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala

290

295

300

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta 1380
Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu

305

310

315

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag 1428
Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys

320

325

330

ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat 1476
Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp

335

340

345

350

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt 1524
Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe

355

360

365

act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa 1572
Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln

370

375

380

ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac	1620
Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn	
385 390 395	

cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct	1668
Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala	
400 405 410	

gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta	1716
Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu	
415 420 425 430	

att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac	1764
Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr	
435 440 445	

atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct	1812
Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala	
450 455 460	

gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt	1860
Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe	
465 470 475	

atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag	1908
Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln	
480 485 490	

agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac	1956
488/735	

Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr
 495 500 505 510

caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct 2004
 Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala
 515 520 525

ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg 2052
 Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val
 530 535 540

gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca 2100
 Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr
 545 550 555

ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag 2148
 Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln
 560 565 570

gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act 2196
 Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr
 575 580 585 590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag 2244
 Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln
 595 600 605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca 2292
 Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro
 489/735

610	615	620	
agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt			2340
Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val			
625	630	635	
gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct			2388
Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala			
640	645	650	
gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa			2436
Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys			
655	660	665	670
gag gca gca gac atg atc cta gtg gat gat gat ttt caa acc ata atg			2484
Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met			
675	680	685	
tct gca atc gaa gag ggt aaa ggg att tat aat aac att aaa aat ttc			2532
Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe			
690	695	700	
gtt aga ttc cag ctg agc acg agt ata gca gca tta act tta atc tca			2580
Val Arg Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser			
705	710	715	
ttg gct aca tta atg aac ttt cct aat cct ctc aat gcc atg cag att			2628
Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile			
720	725	730	

ttg tgg atc aat att att atg gat gga ccc cca gct cag agc ctt gga 2676
 Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly
 735 740 745 750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg 2724
 Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp
 755 760 765

aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca 2772
 Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser
 770 775 780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta 2820
 Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu
 785 790 795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc 2868
 Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys
 800 805 810

ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc 2916
 Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr
 815 820 825 830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964
 Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr
 835 840 845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct 3012
Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro

850 855 860

ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg 3060
Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu

865 870 875

ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att 3108
Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile

880 885 890

ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt 3156
Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser

895 900 905 910

tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt 3203
Ser Thr Ser Ser Ser Phe Leu Glu Val

915

tatttgcaaa ctaggaattg cagtctgagg atcatittaga agggcaagtt caagaggata 3263

tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323

ttaagacttt aacctgctgg cagtcccaaa tgaaattatg caactttgat atcatattcc 3383

ttgatttaaa ttggcttttg tgattgagtg aaactttata aagcatatgg tcagttattt 3443

aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtacaaata 3503

cactatctat cttagataga tatatTTTTT tttatTTTTa aatattgtac tatttatggT 3563

ggTggggcTt tcttactaat acacaaataa atttaatcat ttcaaaggc 3612

<210> 135

<211> 382

<212> PRT

<213> Homo sapiens

<400> 135

Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln

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Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp

20 25 30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser

35 40 45

Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly

50 55 60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr

65 70 75 80

Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn

85 90 95

493/735

Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met
100 105 110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr
115 120 125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys
130 135 140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe
145 150 155 160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln
165 170 175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala
180 185 190

Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys
195 200 205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile
210 215 220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly
225 230 235 240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser
494/735

	245	250	255
Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val			
	260	265	270
Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu			
	275	280	285
Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys			
	290	295	300
Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile			
305	310	315	320
Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr			
	325	330	335
Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala			
	340	345	350
Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr			
	355	360	365
Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp			
	370	375	380

<210> 136

<211> 2467

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (444)..(1589)

<400> 136

acgggagcgc gcgcgggagc tagagagcag tggctcggc gctcgtccgg cccgcagctt 60

cgggtcctca ggcggtgtt gtcgcgaac gggtggttg ggagggggg gtggggggac 120

tctagacagc tgaggcgca aagcgatgag tcctcggctc ttctcctcc ttctccggga 180

cccgtctct gctccctct ccaacgccc gatgatctga gccgcgagg cgccgacagc 240

cgggggccc gacgcagccc ggctcctccc ctctccgcc cttccccag cctgacctg 300

cccgcgctg cagcggtag cctcccccg gctgccgcc tcgccgcgc ggtgacccc 360

tccccggctg ccgccgcgc gcctcggcc gaccaggac ctgccgcct gcggctgctc 420

cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg 473

Met Gly Ala Phe Leu Asp Lys Pro Lys Met

1

5

10

gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta 521

Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu

15

20

25

agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct 569
 Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala

30

35

40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617
 Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val

45

50

55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665
 Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His

60

65

70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713
 Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly

75

80

85

90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg 761
 Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu

95

100

105

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca 809
 Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala

110

115

120

gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat 857
 Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His

125

130

135

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac 905
 Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn
 140 145 150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg 953
 Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu
 155 160 165 170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001
 Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg
 175 180 185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac 1049
 Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr
 190 195 200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097
 Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu
 205 210 215

cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att 1145
 Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile
 220 225 230

atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc 1193
 Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu
 235 240 245 250

tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa 1241
 498/735

Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys

255

260

265

gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac 1289

Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp

270

275

280

aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg 1337

Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser

285

290

295

cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc 1385

Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys

300

305

310

aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta 1433

Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu

315

320

325

330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca 1481

Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro

335

340

345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529

Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr

350

355

360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577

Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

499/735

365

370

375

gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc 1629

Asp Asp Met Trp

380

aaaggagagt acagctcaac ttgttgaaa cttttaacat ccatacctcaa ctttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749

ccagaactga tttttttttt ttttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaaata cagactccag caatttttgt tgtatgattt tgtttttttg 1869

taaagtgtaa ttgtccttgt acaaaatgct catatttaata tatgaactgc tttaaatacac 1929

tatcaaagtt acaagaaatg ttggccttat tgtgtgatgc aacagatata tagccctttc 1989

aagtcatgtt gtgtttggac ttgggggttg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaaat gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaaatgt tcttggtagg ggagttggca ttgttgataa 2169

agccagtcctc ttcatTTAAC tgtctttcag gatgttcctt cgttgtttcc atgagtattg 2229

caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349

tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt 2467

<210> 137

<211> 358

<212> PRT

<213> Homo sapiens

<400> 137

Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val

1 5 10 15

Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp

20 25 30

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu

35 40 45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val

50 55 60

Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg

65 70 75 80

Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn

85 90 95

501/735

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser
100 105 110

Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser
115 120 125

Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met
130 135 140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala
145 150 155 160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser
165 170 175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr
180 185 190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln
195 200 205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln
210 215 220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro
225 230 235 240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln
502/735

	245	250	255
Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln			
	260	265	270
Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr			
	275	280	285
Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln			
	290	295	300
Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly			
305	310	315	320
Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro			
	325	330	335
Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln			
	340	345	350
Pro Gly Pro Gly Tyr Arg			
	355		

<210> 138

<211> 1519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11)..(1084)

<400> 138

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Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn

1

5

10

gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca 97

Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr

15

20

25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata 145

Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile

30

35

40

45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca 193

Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser

50

55

60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa 241

Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys

65

70

75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct 289

Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro

80

85

90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag 337
 Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys
 95 100 105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca 385
 Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala
 110 115 120 125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa 433
 Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys
 130 135 140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca 481
 Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro
 145 150 155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct 529
 Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala
 160 165 170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca 577
 Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro
 175 180 185

cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac 625
 Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr
 190 195 200 205

cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag 673

Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln
210 215 220

cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag 721
Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln
225 230 235

act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca 769
Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro
240 245 250

act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg 817
Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu
255 260 265

cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa 865
Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln
270 275 280 285

act tac act gcc caa act tct cag cct act aat tat act gtg gct cct 913
Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro
290 295 300

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961
Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro
305 310 315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009
Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro
506/735

320	325	330	
agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc			1057
Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly			
335	340	345	
tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc			1104
Tyr Thr Gln Pro Gly Pro Gly Tyr Arg			
350	355		
aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta			1164
ttgaagaagt tcagaaattt aaaagcagag cattttttat gatatcattg ttggtgtaa			1224
ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tccctgctta			1284
aaaatgtagc agcttcttag ttactttgga acactactct tacatgtata aagtgattga			1344
cttgactttc tagcttcct tgtccggagg atattaaaat gctagggatga ggtttagcca			1404
tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa			1464
gatattatgt ataaaatgta acactgatga taggttaata aagatgattg aatcc			1519

<210> 139

<211> 396

<212> PRT

<213> Homo sapiens

<400> 139

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln

1 5 10 15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr

20 25 30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu

35 40 45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp

50 55 60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys

65 70 75 80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro

85 90 95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu

100 105 110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu

115 120 125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg

130 135 140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
145 150 155 160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
165 170 175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val
180 185 190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp
195 200 205

Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro
210 215 220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr
225 230 235 240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
245 250 255

Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
260 265 270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
275 280 285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
290 295 300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr
305 310 315 320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr
325 330 335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala
340 345 350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
355 360 365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe
370 375 380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
385 390 395

<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(1206)

<400> 140

aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta 51

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu

1

5

10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99

Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His

15

20

25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147

Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val

30

35

40

ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa 195

Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys

45

50

55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243

Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser

60

65

70

75

ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat 291

Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn

80

85

90

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga 339

Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg

95

100

105

gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg 387
 Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu
 110 115 120

gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat 435
 Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp
 125 130 135

act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa 483
 Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys
 140 145 150 155

cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta 531
 Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu
 160 165 170

aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta 579
 Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu
 175 180 185

aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt 627
 Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg
 190 195 200

tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca 675
 Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro
 205 210 215

cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa 723
 512/735

Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln
 220 225 230 235

gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca 771
 Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala
 240 245 250

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag 819
 Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln
 255 260 265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag 867
 Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln
 270 275 280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc 915
 Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala
 285 290 295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963
 Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
 300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011
 Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln
 320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059
 Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro
 513/735

335	340	345	
agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct			1107
Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro			
350	355	360	
gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt			1155
Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg			
365	370	375	
aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat			1203
Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr			
380	385	390	395
cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc			1256
Arg			
caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag			1316
cattttttat gatattcattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga			1376
ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttccttag ttactttgga			1436
acactactct tacatgtata aagtgattga cttgactttc tagcttcct tgtccggagg			1496
atattaaaat gctaggggtga ggtttagcca tcttacttgg ctttttacta ttaacatgat			1556
gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga			1616

taggttaata aagatgattg aatcc

1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

1 5 10 15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr

20 25 30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

35 40 45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro

50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly

65 70 75 80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly

85 90 95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val

100 105 110

515/735

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
115 120 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
130 135 140

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
145 150 155 160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
165 170 175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
180 185 190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
195 200 205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
210 215 220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
225 230 235 240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
245 250 255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
516/735

260	265	270
Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala		
275	280	285
Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu		
290	295	300
Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His		
305	310	315
		320
Val Gln Thr		

<210> 142

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)..(1040)

<400> 142

aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggg gccacagag 60

gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro

517/735

1

5

10

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt 158

Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu

15

20

25

cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt 206

Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe

30

35

40

45

gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac 254

Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His

50

55

60

ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg 302

Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg

65

70

75

cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc 350

Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe

80

85

90

cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat 398

Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp

95

100

105

ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc 446

Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg

110

115

120

125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494
Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln

130 135 140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542
Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro

145 150 155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590
Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly

160 165 170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638
Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro

175 180 185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca 686
Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro

190 195 200 205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg 734
Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg

210 215 220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac 782
Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn

225 230 235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac 830
 Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn

240

245

250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc 878
 Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val

255

260

265

cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc 926
 Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu

270

275

280

285

aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg 974
 Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu

290

295

300

agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag 1022
 Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln

305

310

315

ctg acc cat gtg cag aca taggcggcctt cctggccctg gggccggggg 1070
 Leu Thr His Val Gln Thr

320

ctgggggtgtg gggcagtctg ggtcctctca tcaccccccac ttcccaggcc cagcctttcc 1130

aaccctgcct gggatctggg ctttaatgca gaggccatgt ccttgtcttg tctgcttct 1190

ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag 1250

cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg 1310

agaggggagg agtgggcagt gaagatgaag ccccatgctc agtcccctcc catccccac 1370

gcagctccac cccagtccca agccaccagc tgtctgctcc tgggtgggagg tggcctcctc 1430

agccccctct ctctgacctt taacctcact ctcaccttgc accgtgcacc aacccttcac 1490

ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac 1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1

5

10

15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20

25

30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

521/735

35	40	45
Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val		
50	55	60
Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala		
65	70	75 80
Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile		
85	90	95
Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His		
100	105	110
Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe		
115	120	125
Leu Gln Pro Leu Met His Cys Val		
130	135	

<210> 144

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225).. (632)

<400> 144

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ggcgccttcc gtcccgggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggaggggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5

10

15

20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40

45

50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55

60

65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

523/735

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
70 75 80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
85 90 95 100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572
Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser
105 110 115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620
Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu
120 125 130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca 672
Met His Cys Val
135

ttgttaatta gtgacatagt aacatctgta gcagctggtt agtaaaccctc atgtgggggt 732

gggggtggggg tgtattcctt gggggatggt ttgggccgaa tggggagtgg aatatttgac 792

atttttcctg ttttaaattc taggatagat tttaacatcc tttgcgggtcc cagtccaagg 852

taggctgggtg tcatagtctt ctcaactccta atccatgacc actgtttttt tcctatttat 912

atcaccaggt agcctactga gttaatatattt aagttgtcaa tagataagtg tcctgtttt 972

gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta tttcagcttt 1032

gaaaccaaat ctgtgtatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092

ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152

tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212

gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe

20 25 30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln

35 40 45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg

50 55 60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro
65 70 75 80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu
85 90 95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser
100 105 110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu
115 120 125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu
130 135 140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met
145 150 155 160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp
165 170 175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val
180 185 190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu
195 200 205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp
210 215 220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile
225 230 235 240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala
245 250 255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu
260 265 270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe
275 280 285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe
290 295 300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys
305 310 315 320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser
325 330 335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile
340 345 350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met
355 360 365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys
527/735

370

375

380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile

385

390

395

400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala

405

410

415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu

420

425

430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr

435

440

445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala

450

455

460

Ala Ser Gly Ile

465

<210> 146

<211> 1943

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (379)..(1782)

<400> 146

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ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaaatggct ggggcaatta 240

tagaaaacat gagcaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

tcatcgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly

1

5

10

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag 459

Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys

15

20

25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc 507

Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe

30

35

40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt 555

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val

45

50

55

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc 603

Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala

60 65 70 75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag 651

His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys

80 85 90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc 699

Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe

95 100 105

atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg 747

Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg

110 115 120

ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata 795

Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile

125 130 135

aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag 843

Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys

140 145 150 155

gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att 891

Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile

160 165 170

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg 939
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val
175 180 185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile
190 195 200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met
205 210 215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg 1083
Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu
220 225 230 235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag 1131
Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu
240 245 250

cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt 1179
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val
255 260 265

ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa 1227
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln
270 275 280

ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag 1275
531/735

Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu

285

290

295

ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac 1323

Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr

300

305

310

315

ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt 1371

Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser

320

325

330

ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac 1419

Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His

335

340

345

tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg 1467

Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu

350

355

360

gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg 1515

Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr

365

370

375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc 1563

Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala

380

385

390

395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg 1611

Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu

532/735

400	405	410	
atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc			1659
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser			
415	420	425	
aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt			1707
Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe			
430	435	440	
gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc			1755
Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe			
445	450	455	
atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca			1802
Ile Asn Asp Asn Ala Ala Ser Gly Ile			
460	465		
tgtttatcag ctttgcatTT gcagttgtca cagtcacatt gattgtactt gtatacgcac			1862
acaaatacac tcatttagcc tttatctcaa aatgtttaaT ataaggaaaa aagcgtcaac			1922
aataaatatt ctttgagtat t			1943

<210> 147

<211> 460

<212> PRT

<213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly

20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro

35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr

50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr

65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val

85 90 95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu

100 105 110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile

115 120 125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly

130 135 140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
145 150 155 160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
165 170 175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met
180 185 190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp
195 200 205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala
210 215 220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp
225 230 235 240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
245 250 255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg
260 265 270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile
275 280 285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu
290 295 300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg
305 310 315 320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg
325 330 335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu
340 345 350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser
355 360 365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val
370 375 380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val
385 390 395 400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu
405 410 415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys
420 425 430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys
435 440 445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
536/735

450

455

460

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376).. (1755)

<400> 148

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gccttcgctc ccggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagcgccc 120

agaaaggagg cgaggaagga gggagtgtat gagaggaggg agcaaaaagc tcaccctaaa 180

acatttatatt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tcgcctttct ggtgggaggc ttgattgctc cagggcccac aacggcagtg tcctacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser

1

5

10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459
 Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg

15 20 25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507
 Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr

30 35 40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555
 Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe

45 50 55 60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603
 Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys

65 70 75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651
 Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr

80 85 90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699
 Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys

95 100 105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747
 Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile

110 115 120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795

Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His
 125 130 135 140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843
 Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu
 145 150 155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891
 Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr
 160 165 170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939
 Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu
 175 180 185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987
 Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile
 190 195 200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc 1035
 Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly
 205 210 215 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag 1083
 Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu
 225 230 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag 1131
 His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys
 539/735

240	245	250	
caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac			1179
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp			
255	260	265	
atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg			1227
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp			
270	275	280	
act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct			1275
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala			
285	290	295	300
gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt			1323
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe			
305	310	315	
cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg			1371
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met			
320	325	330	
agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag			1419
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys			
335	340	345	
ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc			1467
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe			
350	355	360	

ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc 1515
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile
365 370 375 380

aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563
Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp
385 390 395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611
Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys
400 405 410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659
Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser
415 420 425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707
Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe
430 435 440

agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755
Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
445 450 455 460

tgagtcaaca aggcaacaca tgtttatcag ctttgcatTT gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaatt 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc

1919

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<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

1 5 10 15

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65 70 75 80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85 90 95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100 105 110

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Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115

120

125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser

130

135

140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala

145

150

155

160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

165

170

175

Asp Arg His Lys Met Leu Ser

180

<210> 150

<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120).. (668)

<400> 150

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ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc 119

atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

1 5 10 15

cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20 25 30

tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35 40 45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50 55 60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65 70 75 80

gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85 90 95

tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100 105 110

gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115

120

125

gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser

130

135

140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala

145

150

155

160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

165

170

175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 698

Asp Arg His Lys Met Leu Ser

180

ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctccttcccc 758

tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctccttctcc ctaacttttag 818

aaatgttgta cttggctatt ttgattaggg aagagggatg tggctcttga tctccgttgt 878

cttcttgggt ctttgggggt gaagggaggg ggaaggcagg ccagaaggga atggagacat 938

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 actctgtgc cggccccctc acctgcactt gaggggtctg ggcagtccct cctctcccca 1358
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 atctgaacac cacagccct gtacttgggt tgcctcttgt ccctgaactt cgttgtacca 1478
 gtgcatggag agaaaatttt gtccctcttgt cttagagttg tgtgtaaatc aaggaagcca 1538
 tcattaaatt gttttatttc tctc 1562

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<213> Mus musculus

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<221> CDS

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<400> 151

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cagccaggtc tgtgctgccg cctccagca tctttgcagc aggggacgag gctgtgtggg 120

aggctgtcgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggettatt 180

ctccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc 230

Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly

1

5

10

att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278

Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys

15

20

25

ctg ggg agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc 326

Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala

30

35

40

45

atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg 374

Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu

50

55

60

gag tcc ttg aag atg aac aca gta gcc cag ctg gta gcc cac cag tgg 422

Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp

65

70

75

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gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470

Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser

80

85

90

tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt 518

Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys

95

100

105

ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt 566

Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe

110

115

120

125

gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg 614

Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp

130

135

140

gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca 662

Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro

145

150

155

ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca 710

Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala

160

165

170

gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg 758

Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp

175

180

185

gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac 806
 Gly His Thr Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His
 190 195 200 205

cta gag atc agc cag tca ccc act ctt gcc ttt ctc tct tca cac cat 854
 Leu Glu Ile Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His
 210 215 220

gga acc cat ggg ccc agc aag cta tgt aac aca ccg ctg gac act cag 902
 Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln
 225 230 235

gag cct cag ctt gtc cct gaa ggc tgc caa gaa cct gag gag ata agc 950
 Glu Pro Gln Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser
 240 245 250

tgg cct cca tca gtg gag acc agt gtc tcc tta ggg tta cca cac gaa 998
 Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu
 255 260 265

att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct 1046
 Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro
 270 275 280 285

gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc 1094
 Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys
 290 295 300

aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa 1142

Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu
305 310 315

agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt 1190
Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val
320 325 330

cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct 1238
Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro
335 340 345

gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct 1286
Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro
350 355 360 365

ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca acc tcc 1334
Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser
370 375 380

aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat 1382
Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr
385 390 395

aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt 1430
Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg
400 405 410

att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc 1478
Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe
550/735

415	420	425	
tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa	1526		
Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln			
430	435	440	445
gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc	1574		
Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser			
	450	455	460
ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac	1622		
Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn			
	465	470	475
agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca	1670		
Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro			
	480	485	490
ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc	1718		
Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu			
	495	500	505
cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag	1766		
His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys			
510	515	520	525
gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc	1814		
Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg			
	530	535	540
551/735			

tgg aag aaa gcg cag gag gcc aga acc ctc aag gag cag agc ata cag 1862
 Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln

545 550 555

ctg gag gca gag cgg caa aac gtg gca gcc ata tct gct gcc tac aca 1910
 Leu Glu Ala Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr

560 565 570

gcc tat gtc cat agc tat agg gcc tgg caa gca gag atg aac aaa ctt 1958
 Ala Tyr Val His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu

575 580 585

ggg gtg gct ttt ggg aag aac ttg tca ctg ggg act cca aca ccc agc 2006
 Gly Val Ala Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser

590 595 600 605

tgg ccc gga tgt cca cag cca ata cct tct cat cct cag ggt ggt act 2054
 Trp Pro Gly Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr

610 615 620

cca gtt ttc ccc tat tcc cca cag cct cca tcc ttc cct cag cct cca 2102
 Pro Val Phe Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro

625 630 635

tgc ttc cct cag cct cca tcc ttc cct cag cct cca tcc ttc cca ctg 2150
 Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu

640 645 650

cct cca gtc tct tcc cca cag tcc caa tcc ttt cca tca gcc tcc tcc 2198
 Pro Pro Val Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser
 655 660 665

cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc 2246
 Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala
 670 675 680 685

cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg 2294
 Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly
 690 695 700

gcc cag tca tct gat gac aag act gag tgt tcg gag aac ccc tgt atg 2342
 Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met
 705 710 715

ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag 2387
 Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
 720 725 730

tgaccaggtt ggaccccacc tagatggcta gaggtagaag attggacttc acctgggtcc 2447

ttaaaatgat agtggaggaa gggaacctcg cctgggtccc cagagtagcc agaggactta 2507

gcttgggctc ccacagtggc tattagttgg acccagcttg agaccccaga ggcagggaag 2567

accacaccta taaatcaggc ctgggaaaca tgcagaaacc ccatttgaac agactgtggg 2627

actccaatct gaatcctcta tgtggacaga ggatgatggg gccagaggca cctctgaggt 2687

gccctcagcg cagcctcgta aacttcattc actgtgacac atgctgttca tagggctctct 2747

ctggggagga tgcggtcccg gggcacatag ggagggtcct gttttataa taaagttatt 2807

gacaactg 2815

<210> 152

<211> 732

<212> PRT

<213> Mus musculus

<400> 152

Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly Ile Leu Gly

1 5 10 15

Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys Leu Gly Ser

20 25 30

Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu

35 40 45

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu

50 55 60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met

65 70 75 80

Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser Trp Thr Val

85

90

95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser

100

105

110

Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln

115

120

125

Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys

130

135

140

Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser

145

150

155

160

His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg

165

170

175

Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr

180

185

190

Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile

195

200

205

Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His

210

215

220

Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln

225

230

235

240

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Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser Trp Pro Pro
245 250 255

Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu Ile Ser Val
260 265 270

Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro Asp Ala Leu
275 280 285

Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys Thr Glu Leu
290 295 300

Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu Ser Val Gly
305 310 315 320

Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val Pro Val Gly
325 330 335

Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro Ala Gln Pro
340 345 350

Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro Leu Ser Ser
355 360 365

Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser Thr Ser Pro
370 375 380

Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val
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385	390	395	400
Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu			
	405	410	415
Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu			
	420	425	430
Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile			
	435	440	445
Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys			
	450	455	460
Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr			
465	470	475	480
Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys			
	485	490	495
Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile			
	500	505	510
Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn			
	515	520	525
Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys			
	530	535	540

Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala
545 550 555 560

Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val
565 570 575

His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala
580 585 590

Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly
595 600 605

Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe
610 615 620

Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro
625 630 635 640

Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val
645 650 655

Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro
660 665 670

Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val
675 680 685

Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser
690 695 700

Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met Gly Pro Leu
705 710 715 720

Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
725 730

<210> 153

<211> 2544

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97).. (2232)

<400> 153

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agcttctgct gccggaggct gcacccacct gtgccc atg gcc tgc aca ggc cca 114

Met Ala Cys Thr Gly Pro

1

5

tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag 162

Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys

10

15

20

ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag 210
 Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln

25

30

35

ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa 258
 Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu

40

45

50

act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc 306
 Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala

55

60

65

70

cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca 354
 Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro

75

80

85

gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg 402
 Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu

90

95

100

ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac 450
 Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr

105

110

115

cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg 498
 Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly

120

125

130

gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg 546

560/735

Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly	
135	140 145 150
gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca	594
Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser Asn Leu Gly Cys Leu Pro	
155	160 165
cca tcc tcg gct ttg ccc tct ggg acc agg agc ctc cca cgc ccc att	642
Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg Ser Leu Pro Arg Pro Ile	
170	175 180
gac ggt gtt tcg gac tgg agc caa ggg tgc tcc ctg cga tcc act ggc	690
Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly	
185	190 195
agc cct gcc tcc ctg gcc agc aac ttg gaa atc agc cag tcc cct acc	738
Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu Ile Ser Gln Ser Pro Thr	
200	205 210
atg ccc ttc ctc agc ctg cac cgc agc cca cat ggg ccc agc aag ctc	786
Met Pro Phe Leu Ser Leu His Arg Ser Pro His Gly Pro Ser Lys Leu	
215	220 225 230
tgt gac gac ccc cag gcc agc ttg gtg ccc gag cct gtc ccc ggt ggc	834
Cys Asp Asp Pro Gln Ala Ser Leu Val Pro Glu Pro Val Pro Gly Gly	
235	240 245
tgc cag gag cct gag gag atg agc tgg ccg cca tcg ggg gag att gcc	882
Cys Gln Glu Pro Glu Glu Met Ser Trp Pro Pro Ser Gly Glu Ile Ala	
561/735	

250	255	260	
agc cca cca gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg 930			
Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val			
265	270	275	
gcc cca gat gca acc tcc act ggc ctc cct gat acc ccc gca gct cca 978			
Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro			
280	285	290	
gaa acc agc acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc 1026			
Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly			
295	300	305	310
ccc cag tct ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc 1074			
Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys			
315	320	325	
tct gtc aaa gac cag acg cca ctc caa ctt tct gta gaa gat acc acc 1122			
Ser Val Lys Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr			
330	335	340	
tct cca aat acc aag ccg tgc cca cct act ccc acc acc cca gaa aca 1170			
Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr			
345	350	355	
tcc cct cct cct cct cct cct cct cct tca tct act cct tgt tca gct 1218			
Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala			
360	365	370	

cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg 1266
 His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser
 375 380 385 390

gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa 1314
 Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu
 395 400 405

cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc 1362
 His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro
 410 415 420

gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag 1410
 Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu
 425 430 435

ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta 1458
 Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu
 440 445 450

ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac 1506
 Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn
 455 460 465 470

caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc 1554
 Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val
 475 480 485

atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac 1602
 Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp
 490 495 500

acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag 1650
 Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln
 505 510 515

atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag 1698
 Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln
 520 525 530

gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg 1746
 Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg
 535 540 545 550

gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg 1794
 Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu
 555 560 565

aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca 1842
 Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala
 570 575 580

cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg 1890
 Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly
 585 590 595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc 1938
 564/735

Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro
600 605 610

ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg 1986
Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro
615 620 625 630

cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca 2034
Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro
635 640 645

cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc 2082
Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala
650 655 660

ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc 2130
Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro
665 670 675

ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac 2178
Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His
680 685 690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag 2226
Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu
695 700 705 710

gca gaa tgaccgcgtg tccttgccctg accacctggg gaacaccct ggacccaggc 2282
Ala Glu

atcggccagg accccataga gcaccccggt ctgccctgtg ccctgtggac agtggaagat 2342
 gaggtcatct gccactttca ggacattgtc cgggagccct tcatttagga caaaacgggc 2402
 gcgatgatgc cctggctttc aggggtggta gaactggata cggtgtttac aattccaatc 2462
 tctctatttc tgggtgaagg gtcttggtgg tgggggtatt gctacggtct ttttaattata 2522
 ataaatattt attgaatgct tc 2544

<210> 154

<211> 712

<212> PRT

<213> Homo sapiens

<400> 154

Met Ala Cys Thr Gly Pro Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly

1 5 10 15

Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys Thr

20 25 30

Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu

35 40 45

Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu

50 55 60

Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
65 70 75 80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
100 105 110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
115 120 125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
130 135 140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
145 150 155 160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
165 170 175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
180 185 190

Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
195 200 205

Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
567/735

210	215	220	
His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro			
225	230	235	240
Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro			
	245	250	255
Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro			
	260	265	270
Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro			
	275	280	285
Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys			
	290	295	300
Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu			
305	310	315	320
Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu			
	325	330	335
Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr			
	340	345	350
Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Ser			
	355	360	365

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser

370

375

380

Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu

385

390

395

400

His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu

405

410

415

Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln

420

425

430

Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His

435

440

445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu

450

455

460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln

465

470

475

480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro

485

490

495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg

500

505

510

Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe

515

520

525

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Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln

530

535

540

Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg

545

550

555

560

Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser

565

570

575

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly

580

585

590

Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro

595

600

605

Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp

610

615

620

Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr

625

630

635

640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro

645

650

655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln

660

665

670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln

570/735

675

680

685

Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala Pro

690

695

700

Glu Asp Lys Thr Gln Glu Ala Glu

705

710

<210> 155

<211> 3456

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (281).. (3016)

<400> 155

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cgtgtccacc cggatcatgcc cgccgcgcac cagccccgca gtggacttgg aggaggagga 120

ggaggagagc tctgtggatg gcaaagggga ccggaagagc acaggcctga aactctccaa 180

gaagaaagca aggaggagac acacggatga cccaagcaag gaatgcttca ctctgaaatt 240

tgacctgaat gtggacattg agacagagat cgtcccagcc atg aag aag aag tca 295

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Met Lys Lys Lys Ser

1

5

ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg 343

Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu

10

15

20

ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc 391

Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu

25

30

35

acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc 439

Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala

40

45

50

cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac 487

Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp

55

60

65

tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc 535

Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro

70

75

80

85

ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac 583

Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp

90

95

100

atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg 631

Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly

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105

110

115

gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct 679

Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser

120

125

130

ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag 727

Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys

135

140

145

aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc 775

Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser

150

155

160

165

acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc 823

Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly

170

175

180

aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg 871

Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly

185

190

195

ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag 919

Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu

200

205

210

gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc 967

Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu

215

220

225

att gat ggg cat gag aag ctg acc cgg cgg cag tgc cac cag cag gag 1015

Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu

230 235 240 245

gcg gtg tgg gag ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg 1063

Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu

250 255 260

cgg gtg atc atc aac ctg ttc ttg tgc tgc ctc ctg aac ctg caa gag 1111

Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu

265 270 275

tca ggg ctg ctg tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc 1159

Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile

280 285 290

ccg gag atc gcg cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg 1207

Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala

295 300 305

ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg 1255

Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly

310 315 320 325

gac ttc ctc aaa ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac 1303

Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr

330 335 340

atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc 1351
 Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly

345 350 355

ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag 1399
 Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu

360 365 370

aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa 1447
 Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys

375 380 385

ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg 1495
 Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu

390 395 400 405

agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc 1543
 Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile

410 415 420

ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag 1591
 Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln

425 430 435

cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc 1639
 Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala

440 445 450

tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag 1687

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Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys

455

460

465

gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg 1735

Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro

470

475

480

485

gag gag acg cgg cag ctg ctg ctg gag ggg agc ctg agg atg aag gag 1783

Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu

490

495

500

ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg 1831

Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu

505

510

515

ctg ttg gtg acc aaa gca gtg aag aag gca gag agg acc agg gtc atc 1879

Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile

520

525

530

agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac 1927

Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp

535

540

545

cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta 1975

Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val

550

555

560

565

ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg 2023

Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp

576/735

570	575	580	
gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca			2071
Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala			
585	590	595	
cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag			2119
Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu			
600	605	610	
gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa			2167
Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu			
615	620	625	
ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg			2215
Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg			
630	635	640	645
aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc			2263
Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser			
650	655	660	
acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc			2311
Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser			
665	670	675	
tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc			2359
Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr			
680	685	690	

tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg 2407

Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu

695

700

705

ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac 2455

Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr

710

715

720

725

ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca 2503

Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro

730

735

740

atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc 2551

Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser

745

750

755

cct cca ccc tcg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg 2599

Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu

760

765

770

agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc 2647

Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu

775

780

785

cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc 2695

Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser

790

795

800

805

cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg 2743
 Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg

810 815 820

act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg 2791
 Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly

825 830 835

gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg 2839
 Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly

840 845 850

gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg 2887
 Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly

855 860 865

gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag 2935
 Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln

870 875 880 885

cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg 2983
 His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu

890 895 900

ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gaggccccc 3036
 Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val

905 910

agagtgccat tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc 3096

ttcagctact gcctcctgta tgcattgagcc ggatgctggg caggatccct gcctacgccc 3156

gggcccgatt tgcgctttgc cggactggat ggagtggagg aggcccaggc cacagtacca 3216

ccccacctgc ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag 3276

tcttcagggc tgggctccta ggctgcccatt cctacttcta ccctcactgg cctccagtgg 3336

gattcactcc tgccctgccc ccaccttccc agtcccacag gccacccctg gcttgggctg 3396

ggttctgtga agttacgtat ttattgagct tttggttctt ttataaagac ttgtctagac 3456

<210> 156

<211> 912

<212> PRT

<213> Homo sapiens

<400> 156

Met Lys Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg

1 5 10 15

Lys Gly Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn

20 25 30

Thr Pro Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr

35 40 45

Leu Arg Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu
50 55 60

Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro
65 70 75 80

Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg
85 90 95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met
100 105 110

Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr
115 120 125

Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr
130 135 140

Gly Asp Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe
145 150 155 160

Ser Ser Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met
165 170 175

Glu Gln Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro
180 185 190

Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu
195 200 205

Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp
210 215 220

Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln
225 230 235 240

Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser
245 250 255

Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu
260 265 270

Leu Asn Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg
275 280 285

Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp
290 295 300

Ala Ser Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala
305 310 315 320

Leu Leu Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser
325 330 335

Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met
340 345 350

Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr
582/735

355	360	365
Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser		
370	375	380
Asp Met Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu		
385	390	395 400
Leu Lys Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala		
405	410	415
Val Val Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn		
420	425	430
Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val		
435	440	445
Ser Arg Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val		
450	455	460
Asp Lys Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile		
465	470	475 480
Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser		
485	490	495
Leu Arg Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe		
500	505	510

Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu
515 520 525

Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys
530 535 540

Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu
545 550 555 560

Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala
565 570 575

Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu
580 585 590

Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln
595 600 605

Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu
610 615 620

Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser
625 630 635 640

Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys
645 650 655

Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro
660 665 670

584/735

Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser
675 680 685

Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro
690 695 700

Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser
705 710 715 720

Met Asp Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe
725 730 735

Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser
740 745 750

Pro Arg Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr
755 760 765

Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser
770 775 780

Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr
785 790 795 800

Pro Ser Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro
805 810 815

Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser
585/735

820	825	830
Trp Asp Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val		
835	840	845
Gly Cys Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly		
850	855	860
Asp Leu Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro		
865	870	875
		880
Gly Val Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg		
885	890	895
Ile Arg Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val		
900	905	910

<210> 157

<211> 3609

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (152).. (3169)

<400> 157

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ggatgtatgt caccacgccg actgccagca gctgcaccgc cgggggcccc tcaacctctg 120

cgaggcctgt gacagcaagt tccacagcac c atg cat tat gat ggg cat gtc 172

Met His Tyr Asp Gly His Val

1

5

cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc 220

Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser

10

15

20

acc cgg tca tgc ccg ccg cgc acc agc ccc gca gtg gac ttg gag gag 268

Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu

25

30

35

gag gag gag gag agc tct gtg gat ggc aaa ggg gac cgg aag agc aca 316

Glu Glu Glu Glu Ser Ser Val Asp Gly Lys Gly Asp Arg Lys Ser Thr

40

45

50

55

ggc ctg aaa ctc tcc aag aag aaa gca agg agg aga cac acg gat gac 364

Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp

60

65

70

cca agc aag gaa tgc ttc act ctg aaa ttt gac ctg aat gtg gac att 412

Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile

75

80

85

gag aca gag atc gtc cca gcc atg aag aag aag tca ctg ggg gag gtg 460

587/735

Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val

90

95

100

ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac 508

Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp

105

110

115

atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc acc ttc gag gcc 556

Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala

120

125

130

135

tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc cca gcc aag cct 604

Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala Pro Ala Lys Pro

140

145

150

gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg 652

Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu

155

160

165

agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc ccc gcc ctg gag 700

Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu

170

175

180

cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct 748

Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro

185

190

195

ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg gag gcg agc atc 796

Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile

588/735

200	205	210	215	
ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct ctg ccc agc ggc	844			
Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser Leu Pro Ser Gly				
220	225	230		
agc agt ggc agc acc aac act ggc gac agc tgg aag aac cgg gcg gcc	892			
Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys Asn Arg Ala Ala				
235	240	245		
agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc acc agc gcc ttt	940			
Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe				
250	255	260		
ggc cgg gag gta gac aag atg gag cag ctg gag ggc aag ctg cac acc	988			
Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr				
265	270	275		
tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg ctg cgc ttc gac	1036			
Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly Leu Arg Phe Asp				
280	285	290	295	
cat gac tcc tgg gag gag gag tac gat gaa gac gag gat gag gac aat	1084			
His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu Asp Glu Asp Asn				
300	305	310		
gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat	1132			
Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His				
315	320	325		

gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag 1180
 Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu

330

335

340

ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc 1228
 Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile

345

350

355

aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg 1276
 Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu

360

365

370

375

tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc ccg gag atc gcg 1324
 Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala

380

385

390

cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag 1372
 Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu

395

400

405

aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa 1420
 Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys

410

415

420

ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac atc cgc tac tgc 1468
 Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys

425

430

435

atg gag gag gag ggc tgc atg gag tac atg cgc ggc ctg ctg cgc gac 1516
 Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp
 440 445 450 455

aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag aag cac cca cag 1564
 Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu Lys His Pro Gln
 460 465 470

tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa ccc cac cag cgg 1612
 Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg
 475 480 485

ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg agg aag acc gag 1660
 Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu
 490 495 500

gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc ggc tcc gtg gag 1708
 Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu
 505 510 515

cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg 1756
 Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg
 520 525 530 535

cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc tac gag gtg gtg 1804
 Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val
 540 545 550

gaa agc agc agc gac gaa gtg gac aag ctc ctg aag gaa ttt ctg cac 1852
 591/735

Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys Glu Phe Leu His

555

560

565

ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg gag gag acg cgg 1900

Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro Glu Glu Thr Arg

570

575

580

cag ctg ctg ctg gag ggg agc ctg agg atg aag gag ggg aag gac agc 1948

Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu Gly Lys Asp Ser

585

590

595

aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg ctg ttg gtg acc 1996

Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr

600

605

610

615

aaa gca gtg aag aag gca gag agg acc agg gtc atc agg cca ccc ctg 2044

Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile Arg Pro Pro Leu

620

625

630

ctc gtg gac aag att gtg tgc cgg gag cta cgg gac cct ggg tcc ttc 2092

Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp Pro Gly Ser Phe

635

640

645

ctc ctt atc tac ctg aat gag ttt cac agt gct gta ggg gcc tac acg 2140

Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val Gly Ala Tyr Thr

650

655

660

ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg gtg gac acc att 2188

Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp Val Asp Thr Ile

592/735

665	670	675	
tac aat gcc cag aac cag ctg caa cag ctg cgt gca cag gag ccc cca	2236		
Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala Gln Glu Pro Pro			
680	685	690	695
ggc agt cag cag ccc ctg cag agc ctg gaa gag gag gag gat gag cag	2284		
Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu Glu Asp Glu Gln			
700	705	710	
gag gag gaa gag gag gag gag gag gag gag gag gaa ggc gag gac agt	2332		
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Glu Asp Ser			
715	720	725	
ggc act tca gct gcc agc tcc cct acc atc atg cgg aaa agc agc ggc	2380		
Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg Lys Ser Ser Gly			
730	735	740	
agc ccc gac tct cag cac tgt gcc tca gat ggc tcc acg gag acc ctg	2428		
Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser Thr Glu Thr Leu			
745	750	755	
gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc tcc ccc gag ttc	2476		
Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser Ser Pro Glu Phe			
760	765	770	775
gac agc ggt cct ttc agc tcc cag tct gat gag acc tct ctc agc acc	2524		
Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr Ser Leu Ser Thr			
780	785	790	

act gcc tca tct gcc acg ccc acc agt gag ctg ctg ccc ctg ggt ccg 2572
 Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro

795

800

805

gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac ggc acc ctc tcc 2620
 Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr Gly Thr Leu Ser

810

815

820

cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta 2668
 Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro Met Ala Glu Leu

825

830

835

gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc cct cca ccc tcg 2716
 Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser
 840 845 850 855

ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg agc tgc ccg ccc 2764
 Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro

860

865

870

cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc cag ctg ctg gca 2812
 His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala

875

880

885

ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc cgc agc ctg tca 2860
 Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser Arg Ser Leu Ser

890

895

900

gag ctc tgc ctg gct gtt cca gcc cca ggt att agg act cag ggc tcc 2908

Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg Thr Gln Gly Ser

905

910

915

cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg gcc cct agc cct 2956

Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly Ala Pro Ser Pro

920

925

930

935

ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg gaa cct gca ggc 3004

Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly Glu Pro Ala Gly

940

945

950

tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg gcc tct ccc agg 3052

Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly Ala Ser Pro Arg

955

960

965

gtc cag cct gag ccc cca cca ggg gtc tct gcc cag cac agg aag ctg 3100

Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln His Arg Lys Leu

970

975

980

acc ctg gcc cag ctc tac cga atc agg acc acc ctg ctg ctt aac tcc 3148

Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser

985

990

995

acg ctc act gcc tcg gag gtc tgagcagagg gaggcccca agagtgccat 3199

Thr Leu Thr Ala Ser Glu Val

1000

1005

tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc ttcagctact 3259

595/735

gcctcctgta tgcattgagcc ggatgctggg caggatccct gcctacgccc gggcccgatt 3319

tcgcttttgc cggactggat ggagtggagg aggcccaggc cacagtacca cccacactgc 3379

ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag tcttcagggc 3439

tgggctccta ggctgcccatt cctacttcta ccctcactgg cctccagtgg gattcactcc 3499

tgccctgccc ccacattccc agtcccacag gccaccctg gcttgggctg ggttctgtga 3559

agttacgtat ttattgagct ttgtgttctt ttataaagac ttgtctagac 3609

<210> 158

<211> 1006

<212> PRT

<213> Homo sapiens

<400> 158

Met His Tyr Asp Gly His Val Arg Phe Asp Leu Pro Pro Gln Gly Ser

1 5 10 15

Val Leu Ala Arg Asn Val Ser Thr Arg Ser Cys Pro Pro Arg Thr Ser

20 25 30

Pro Ala Val Asp Leu Glu Glu Glu Glu Glu Ser Ser Val Asp Gly

35 40 45

Lys Gly Asp Arg Lys Ser Thr Gly Leu Lys Leu Ser Lys Lys Lys Ala
50 55 60

Arg Arg Arg His Thr Asp Asp Pro Ser Lys Glu Cys Phe Thr Leu Lys
65 70 75 80

Phe Asp Leu Asn Val Asp Ile Glu Thr Glu Ile Val Pro Ala Met Lys
85 90 95

Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly
100 105 110

Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro
115 120 125

Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg
130 135 140

Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly
145 150 155 160

Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly
165 170 175

Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu
180 185 190

Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu
195 200 205

Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser
210 215 220

Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp
225 230 235 240

Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser
245 250 255

Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln
260 265 270

Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu
275 280 285

Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp
290 295 300

Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp
305 310 315 320

Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His
325 330 335

Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile
340 345 350

Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn
598/735

355	360	365
Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe		
370	375	380
Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser		
385	390	395 400
Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu		
405	410	415
Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe		
420	425	430
Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr		
435	440	445
Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr		
450	455	460
Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met		
465	470	475 480
Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys		
485	490	495
Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val		
500	505	510

Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys
515 520 525

Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg
530 535 540

Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys
545 550 555 560

Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly
565 570 575

Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg
580 585 590

Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe
595 600 605

Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr
610 615 620

Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu
625 630 635 640

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His
645 650 655

Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys
660 665 670
600/735

Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln
675 680 685

Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu
690 695 700

Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu
705 710 715 720

Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr
725 730 735

Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser
740 745 750

Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp
755 760 765

Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser
770 775 780

Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser
785 790 795 800

Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp
805 810 815

Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala
601/735

820	825	830
Pro Gly Pro Met Ala Glu Leu Val	Pro Arg Ala Pro Glu Ser Pro Arg	
835	840	845
Val Pro Ser Pro Pro Pro Ser	Pro Arg Leu Arg Arg Arg Thr Pro Val	
850	855	860
Gln Leu Leu Ser Cys Pro Pro His	Leu Leu Lys Ser Lys Ser Glu Ala	
865	870	875 880
Ser Leu Leu Gln Leu Leu Ala Gly	Ala Gly Thr His Gly Thr Pro Ser	
885	890	895
Ala Pro Ser Arg Ser Leu Ser Glu	Leu Cys Leu Ala Val Pro Ala Pro	
900	905	910
Gly Ile Arg Thr Gln Gly Ser Pro	Gln Glu Ala Gly Pro Ser Trp Asp	
915	920	925
Cys Arg Gly Ala Pro Ser Pro Gly	Ser Gly Pro Gly Leu Val Gly Cys	
930	935	940
Leu Ala Gly Glu Pro Ala Gly Ser	His Arg Lys Arg Cys Gly Asp Leu	
945	950	955 960
Pro Ser Gly Ala Ser Pro Arg Val	Gln Pro Glu Pro Pro Pro Gly Val	
965	970	975

Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg

980

985

990

Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val

995

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1005

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Met Gly Trp Lys Pro Ser Glu

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gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

10

15

20

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga 209

603/735

Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
25 30 35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val
40 45 50 55

ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac 305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
60 65 70

ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc 353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
75 80 85

agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc 401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
90 95 100

acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg 449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
105 110 115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
120 125 130 135

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg
604/735

140	145	150	
gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag			593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys			
155	160	165	
cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc			641
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg			
170	175	180	
cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg			689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg			
185	190	195	
ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg			737
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp			
200	205	210	215
ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc			785
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile			
220	225	230	
cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg			833
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp			
235	240	245	
gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg			881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val			
250	255	260	

gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac	929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp	
265 270 275	
 cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt	977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser	
280 285 290 295	
 gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg	1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu	
300 305 310	
 gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac	1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn	
315 320 325	
 ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc	1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile	
330 335 340	
 acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg	1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp	
345 350 355	
 acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc	1217
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly	
360 365 370 375	

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 Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln

380 385 390

gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc 1313
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395 400 405

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 Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala

410 415 420

gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac 1409
 Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr

425 430 435

cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag 1457
 Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu

440 445 450 455

aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag 1505
 Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys

460 465 470

agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt 1553
 Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly

475 480 485

aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg 1601

607/735

Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val

490

495

500

gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg 1649

Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu

505

510

515

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg 1697

Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val

520

525

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535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg 1745

Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu

540

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ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg 1793

Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg

555

560

565

gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg 1841

Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val

570

575

580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt 1889

Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys

585

590

595

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc 1937

Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala

608/735

600	605	610	615	
atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag				1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu				
	620	625	630	
gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg				2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu				
	635	640	645	
ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att				2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile				
	650	655	660	
ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc				2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe				
	665	670	675	
acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag				2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln				
	680	685	690	695
atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag				2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys				
	700	705	710	
ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg				2273
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu				
	715	720	725	
609/735				

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag 2321
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu

730 735 740

gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu

745 750 755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417
Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu

760 765 770 775

ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg 2465
Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr

780 785 790

gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg 2513
Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val

795 800 805

agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag 2561
Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu

810 815 820

ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag 2609
Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu

825 830 835

cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg 2657
 Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
 840 845 850 855

acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc 2705
 Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
 860 865 870

gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg 2753
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 875 880 885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg 2801
 Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
 890 895 900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc 2849
 Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg
 905 910 915

cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg 2897
 Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
 920 925 930 935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945
 Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu
 940 945 950

cgc atc acc tgc ccc atc tgc atc gac agg cac atc cgc ctc gtg ttc 2993

Arg Ile Thr Cys Pro Ile Cys Ile Asp Arg His Ile Arg Leu Val Phe

955

960

965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041

Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala

970

975

980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089

Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val

985

990

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3168

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30

Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp

612/735

35

40

45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp

50

55

60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val

65

70

75

80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val

85

90

95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr

100

105

110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val

115

120

125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg

130

135

140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr

145

150

155

160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg

165

170

175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly

180

185

190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val
195 200 205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys
210 215 220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg
225 230 235 240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg
245 250 255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala
260 265 270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala
275 280 285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly
290 295 300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln
305 310 315 320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln
325 330 335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
340 345 350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
355 360 365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu
370 375 380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
385 390 395 400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly
405 410 415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
420 425 430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
435 440 445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu
450 455 460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
465 470 475 480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
485 490 495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala
615/735

500	505	510
Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu		
515	520	525
Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr		
530	535	540
Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val		
545	550	555
		560
Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser		
565	570	575
Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg		
580	585	590
Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser		
595	600	605
Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly		
610	615	620
Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr		
625	630	635
		640
Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His		
645	650	655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
660 665 670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
675 680 685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
690 695 700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
705 710 715 720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
725 730 735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
740 745 750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
755 760 765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
770 775 780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
785 790 795 800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
805 810 815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly

820

825

830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro

835

840

845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His

850

855

860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser

865

870

875

880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val

885

890

895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val

900

905

910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala

915

920

925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser

930

935

940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp

945

950

955

960

Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro

618/735

965

970

975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg

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985

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Asp Arg Ile Gln Ile Phe Val

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cactggcgcg atgcgggccg tcctctcggc tg atg ggt tgg aag ccc agc gag 113

Met Gly Trp Lys Pro Ser Glu

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gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

10

15

20

619/735

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga	209
Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg	
25 30 35	
gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg	257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val	
40 45 50 55	
ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac	305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp	
60 65 70	
ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc	353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly	
75 80 85	
agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc	401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly	
90 95 100	
acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg	449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu	
105 110 115	
ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt	497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys	
120 125 130 135	

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545
 Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg

140 145 150

gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag 593
 Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys

155 160 165

cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc 641
 His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg

170 175 180

cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg 689
 Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg

185 190 195

ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg 737
 Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp

200 205 210 215

ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc 785
 Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile

220 225 230

cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg 833
 Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp

235 240 245

gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg 881

621/735

Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val

250

255

260

gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac 929

Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp

265

270

275

cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt 977

His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser

280

285

290

295

gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg 1025

Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu

300

305

310

gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac 1073

Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn

315

320

325

ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc 1121

Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile

330

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340

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Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp

345

350

355

acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc 1217

Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly

622/735

360	365	370	375	
gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag				1265
Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln				
	380	385	390	
gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc				1313
Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg				
	395	400	405	
gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca				1361
Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala				
	410	415	420	
gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac				1409
Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr				
	425	430	435	
cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag				1457
Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu				
	440	445	450	455
aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag				1505
Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys				
	460	465	470	
agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt				1553
Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly				
	475	480	485	
623/735				

aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg 1601
 Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val

490 495 500

gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg 1649
 Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu

505 510 515

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg 1697
 Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val

520 525 530 535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg 1745
 Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu

540 545 550

ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg 1793
 Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg

555 560 565

gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg 1841
 Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val

570 575 580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag-cgc ggc tgt 1889
 Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys

585 590 595

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc 1937
 Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala
 600 605 610 615

atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag 1985
 Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
 620 625 630

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg 2033
 Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
 635 640 645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att 2081
 Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
 650 655 660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc 2129
 Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
 665 670 675

acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag 2177
 Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
 680 685 690 695

atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag 2225
 Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys
 700 705 710

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg 2273
 625/735

Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu

715

720

725

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag 2321

Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu

730

735

740

gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369

Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu

745

750

755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417

Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu

760

765

770

775

ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg 2465

Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr

780

785

790

gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg 2513

Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val

795

800

805

agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag 2561

Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu

810

815

820

ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag 2609

Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu

626/735

825	830	835	
cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg	2657		
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly			
840	845	850	855
acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc	2705		
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro			
	860	865	870
gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg	2753		
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu			
	875	880	885
ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg	2801		
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg			
	890	895	900
atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc	2849		
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg			
	905	910	915
cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg	2897		
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro			
	920	925	930
cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa	2945		
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu			
	940	945	950

cgc atc acc tgc ccc atc tgc atc gac agc cac atc cgc ctc gtg ttc 2993

Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe

955

960

965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041

Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala

970

975

980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089

Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val

985

990

995

tgagccgcgc cgtccgcgc gcccgagctg ccttcgcgtg cccccgccct gtgttttata 3149

aaaagaaaga ttctcgat

3168

<210> 162

<211> 999

<212> PRT

<213> Homo sapiens

<400> 162

Met Gly Trp Lys Pro Ser Glu Ala Arg Gly Gln Ser Gln Ser Leu Gln

1

5

10

15

Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr

20

25

30

628/735

Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp
35 40 45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
50 55 60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
65 70 75 80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
85 90 95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
100 105 110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
115 120 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
130 135 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
145 150 155 160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
165 170 175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
629/735

	180		185		190
Leu	Pro	Arg	Ile	Pro	Leu
Arg	Gly	Ile	Phe	Gln	Gly
Ala	Lys	Val	Val		
	195		200		205
Arg	Gly	Pro	Phe	Trp	Glu
Trp	Gly	Ser	Gln	Asp	Gly
Gly	Glu	Gly	Lys		
	210		215		220
Pro	Gly	Arg	Val	Val	Asp
Ile	Arg	Gly	Trp	Asp	Val
Glu	Thr	Gly	Arg		
	225		230		235
					240
Ser	Val	Ala	Ser	Val	Thr
Trp	Ala	Asp	Gly	Thr	Thr
Asn	Val	Tyr	Arg		
	245		250		255
Val	Gly	His	Lys	Gly	Lys
Val	Asp	Leu	Lys	Cys	Val
Gly	Glu	Ala	Ala		
	260		265		270
Gly	Gly	Phe	Tyr	Tyr	Lys
Asp	His	Leu	Pro	Arg	Leu
Gly	Lys	Pro	Ala		
	275		280		285
Glu	Leu	Gln	Arg	Arg	Val
Ser	Ala	Asp	Ser	Gln	Pro
Phe	Gln	His	Gly		
	290		295		300
Asp	Lys	Val	Lys	Cys	Leu
Leu	Asp	Thr	Asp	Val	Leu
Arg	Glu	Met	Gln		
	305		310		315
					320
Glu	Gly	His	Gly	Gly	Trp
Asn	Pro	Arg	Met	Ala	Glu
Phe	Ile	Gly	Gln		
	325		330		335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln

340

345

350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys

355

360

365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu

370

375

380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp

385

390

395

400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly

405

410

415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser

420

425

430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp

435

440

445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu

450

455

460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu

465

470

475

480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu

485

490

495

631/735

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala
500 505 510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
515 520 525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
530 535 540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
545 550 555 560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
565 570 575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
580 585 590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
595 600 605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
610 615 620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
625 630 635 640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
632/735

645	650	655
Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp		
660	665	670
Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn		
675	680	685
Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp		
690	695	700
Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val		
705	710	715
Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys		
725	730	735
Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala		
740	745	750
Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly		
755	760	765
Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu		
770	775	780
Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu		
785	790	795
		800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
805 810 815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
820 825 830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
835 840 845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
850 855 860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
865 870 875 880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
885 890 895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
900 905 910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
915 920 925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
930 935 940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
945 950 955 960

Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro

965

970

975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg

980

985

990

Asp Arg Ile Gln Ile Phe Val

995

<210> 163

<211> 4031

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (91)..(2649)

<400> 163

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tcccgtcgcc aatccccgcc gtcccgggcc atg atc gcc tgg cgt ctg ccc ttg 114

Met Ile Ala Trp Arg Leu Pro Leu

1

5

tgc gtg ctc ttg gtg gcc tcc gtc gag agc cac ctg ggg gcc ctg ggg 162

635/735

Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly

10

15

20

ccc aag aac gtc tcg cag aaa gac gcg gag ttt gag cgc acc tac gcg 210

Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala

25

30

35

40

gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc 258

Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr

45

50

55

gtg acc cgc aac cgg acc gag ggt gtg cga gtg tct gtg aat gtc ctg 306

Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu

60

65

70

aac aag cag aaa ggg gcg cct ttg ctg ttc gtg gtc cgc cag aag gag 354

Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu

75

80

85

gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag 402

Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln

90

95

100

cgg aag tac ctc tac caa aaa gtg gaa cga act ctg tgt cag ccc ccc 450

Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro

105

110

115

120

acc aag aat gag tct gag atc cag ttt ttc tat gtg gac gtg tct acc 498

Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr

636/735

125	130	135	
ctg tca ccc gtc aat acc act tac cag ctc cga gtc aac cgt gtg gac	546		
Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Asn Arg Val Asp			
140	145	150	
aat ttt gtg ctc agg act gga gag ctg ttt acc ttt aat acc act gca	594		
Asn Phe Val Leu Arg Thr Gly Glu Leu Phe Thr Phe Asn Thr Thr Ala			
155	160	165	
gcc cag ccc cag tac ttc aaa tac gag ttt cct gat ggt gtg gac tcg	642		
Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Asp Gly Val Asp Ser			
170	175	180	
gta att gtc aag gtg acc tcc aag aag gcc ttc ccc tgc tca gtc atc	690		
Val Ile Val Lys Val Thr Ser Lys Lys Ala Phe Pro Cys Ser Val Ile			
185	190	195	200
tcc atc cag gat gtc ctg tgc cct gtc tat gat ctg gac aac agt gta	738		
Ser Ile Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Ser Val			
205	210	215	
gcc ttc att ggc atg tac cag acg atg act aag aag gca gcc atc act	786		
Ala Phe Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr			
220	225	230	
gtg cag cgg aaa gac ttc ccc agc aac agc ttc tat gtg gtg gtg gta	834		
Val Gln Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val			
235	240	245	

gtg aag act gag gac cag gcc tgc gga ggg tcc ttg ccc ttc tac cct 882

Val Lys Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro

250

255

260

ttt gtg gaa gat gag cca gtg gat caa ggg cac cgt cag aaa aca ctg 930

Phe Val Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu

265

270

275

280

tca gtg ctg gtc tct cag gct gtc aca tct gag gcc tat gtt ggt ggg 978

Ser Val Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Gly Gly

285

290

295

atg ctc ttt tgc ctg ggc ata ttc ttg tcc ttc tac ctg ctg act gtg 1026

Met Leu Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val

300

305

310

ctg ctg gcc tgt tgg gag aac tgg agg caa agg aag aag acc ttg ctg 1074

Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Arg Lys Lys Thr Leu Leu

315

320

325

gtg gcc ata gac cga gcc tgc cca gaa agt ggt cac gct cgg gtc ttg 1122

Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Ala Arg Val Leu

330

335

340

gct gat tca ttt cct ggc agt gcc cct tac gag ggt tac aac tat ggc 1170

Ala Asp Ser Phe Pro Gly Ser Ala Pro Tyr Glu Gly Tyr Asn Tyr Gly

345

350

355

360

tcc ttt gaa aat ggt tcc gga tcc act gac ggg ttg gtt gaa agc gca 1218

Ser Phe Glu Asn Gly Ser Gly Ser Thr Asp Gly Leu Val Glu Ser Ala

365

370

375

ggt tca ggg gac ctc tcc tac agt tac cag ggg cac gac cag ttc aag 1266

Gly Ser Gly Asp Leu Ser Tyr Ser Tyr Gln Gly His Asp Gln Phe Lys

380

385

390

cgg cgc ctt ccc tct ggc cag atg cgg cag ctg tgc att gcc atg gac 1314

Arg Arg Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Asp

395

400

405

cgc tcc ttt gac gca gtg ggt cct cgg cct cga ctg gac tcc atg agc 1362

Arg Ser Phe Asp Ala Val Gly Pro Arg Pro Arg Leu Asp Ser Met Ser

410

415

420

tcc gtg gaa gag gat gac tac gac acg ctg act gac atc gac tca gac 1410

Ser Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp

425

430

435

440

aaa aac gtc att cga acc aag caa tac ctc tgt gtg gct gat ctg gca 1458

Lys Asn Val Ile Arg Thr Lys Gln Tyr Leu Cys Val Ala Asp Leu Ala

445

450

455

cga aag gac aaa cgt gtt ttg cgg aaa aag tac cag att tac ttc tgg 1506

Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp

460

465

470

aac ata gcc acc att gcg gtc ttc tac gca ctt cct gtg gtg cag ctg 1554

639/735

Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu

475

480

485

gtg atc acc tac cag acg gtg gtg aat gtc aca ggg aac cag gac atc 1602

Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile

490

495

500

tgc tac tac aac ttc ctc tgt gcc cac ccg ctg ggc aac ctc agc gcc 1650

Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala

505

510

515

520

ttc aac aac atc ctc agc aac ttg ggg tac atc ctg ctg ggg ctg ctc 1698

Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu

525

530

535

ttc ctg ctc atc atc ctg cag cga gag atc aat cat aac cgg gcc ctg 1746

Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu

540

545

550

ctg cgg aat gac ctc tat gct ctg gag tgt ggg atc ccc aaa cac ttt 1794

Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe

555

560

565

ggt ctg ttt tac gcc atg ggc aca gca ctg atg atg gag ggg cta ctt 1842

Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu

570

575

580

agt gcc tgt tac cac gtc tgc ccc aac tac acc aac ttc cag ttt gat 1890

Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp

640/735

585	590	595	600	
acc tcc ttc atg tac atg att gct ggc ctc tgc atg ctg aag ctc tac				1938
Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr				
	605	610	615	
cag aag cgg cac cca gat atc aac gcc agt gcc tac agt gca tat gcc				1986
Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala				
	620	625	630	
tgc ttg gcc atc gtc atc ttc ttc tcc gtt ctg ggc gtg gtg ttt ggc				2034
Cys Leu Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly				
	635	640	645	
aaa ggg aac acg gcc ttc tgg att gtc ttc tcc gtc att cac atc atc				2082
Lys Gly Asn Thr Ala Phe Trp Ile Val Phe Ser Val Ile His Ile Ile				
	650	655	660	
tcc acc ctg ctc ctc agc act cag ctc tat tac atg ggc cgc tgg aag				2130
Ser Thr Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys				
665	670	675	680	
ctg gac ttc ggg atc ttc cgc cgc atc ctc cat gtg ctc tac aca gac				2178
Leu Asp Phe Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp				
	685	690	695	
tgc atc cgg cag tgc agc ggg ccc ctt tac acg gac cgc atg gtg ctt				2226
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Thr Asp Arg Met Val Leu				
	700	705	710	
641/735				

ctg gtc atg ggc aac att atc aac tgg tcg ctg gct gca tac gga ctc 2274
 Leu Val Met Gly Asn Ile Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu

715 720 725

atc atg cgc ccc aat gac ttt gct tcc tac ttg ctg gca att ggc atc 2322
 Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile

730 735 740

tgc aac ctg ctg ctt tat ttc gcc ttc tac atc atc atg aag ctc cgg 2370
 Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg

745 750 755 760

agc ggc gag agg atc aag ctc atc cct ctg ctt tgc atc gtc tgc acc 2418
 Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr

765 770 775

tcc gtg gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctg agc 2466
 Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser

780 785 790

acg tgg cag aaa acc ccc gca gag tcc agg gag cac aac cgc gac tgc 2514
 Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys

795 800 805

atc ctc ctc gac ttc ttt gat gac cac gat atc tgg cac ttc ctg tcc 2562
 Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser

810 815 820

tcc att gcc atg ttt ggg tcc ttc ctg gtt ttg ctg acg ttg gat gac 2610
 Ser Ile Ala Met Phe Gly Ser Phe Leu Val Leu Leu Thr Leu Asp Asp
 825 830 835 840

gac ttg gac aca gta cag cgg gac aag atc tat gtc ttc tagcagcatc 2659
 Asp Leu Asp Thr Val Gln Arg Asp Lys Ile Tyr Val Phe
 845 850

tgtggtccag gcttcacctc acgggcctag cgcctgcctc tgcatacct gccagttgcc 2719

acaagaacac cacgggtgtg agtcccagct ctgctgccca gcattggatg tcgtggcaag 2779

acagcgagat tccagcccag gcctgactca ggacagttcc tggtaggact gagccttgga 2839

gttgctctg cggaggagga ggctgtctcc gcattcccca gacactggcc aaattgctgc 2899

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actggctctc catttgctcc tttggagagg aaggtaggaa ggcaatgtcc tgtccattt 3019

catgccttgc attctgccca tcccttcct cctctcagct taggacacac agccctttct 3079

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cagtgagggc cagcccaagt tgagtcttct gatcggggac tgaattcaga ggccaccta 3379

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ccagctcttg cccctggcca ttctggctct tggcgtttac agagtcaccc agtccaggc 3799

ccctggccac tttgtactt ggttgccctt cacttcacca ggtccattcc agatgccaa 3859

agtgggcccc aggaatgtgt ttctttctct ccacatgtt tttatagctc ttgggctggg 3919

agaagaggcg ggtctgggtc ttgtttctg agctttgttc tatgttcctc catgctacgg 3979

ttgcaattgt tttctatgaa cgagtacatt caataaagac aaccagacct gg 4031

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<212> PRT

<213> Mus musculus

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20 25 30

Ala Glu Phe Glu Arg Thr Tyr Ala Asp Asp Val Asn Ser Glu Leu Val
35 40 45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
50 55 60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
65 70 75 80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
85 90 95

Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val
100 105 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
115 120 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
130 135 140

645/735

Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu
145 150 155 160

Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
165 170 175

Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys
180 185 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
195 200 205

Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr
210 215 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225 230 235 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
245 250 255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp
260 265 270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
275 280 285

Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe
646/735

290	295	300	
Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp			
305	310	315	320
Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro			
	325	330	335
Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala			
	340	345	350
Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser			
	355	360	365
Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser			
	370	375	380
Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met			
385	390	395	400
Arg Gln Leu Cys Ile Ala Met Asp Arg Ser Phe Asp Ala Val Gly Pro			
	405	410	415
Arg Pro Arg Leu Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp			
	420	425	430
Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln			
	435	440	445

Tyr Leu Cys Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
450 455 460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
465 470 475 480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
485 490 495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
500 505 510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
515 520 525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
530 535 540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Tyr Ala Leu
545 550 555 560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
565 570 575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
580 585 590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
595 600 605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
610 615 620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
625 630 635 640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
645 650 655

Val Phe Ser Val Ile His Ile Ile Ser Thr Leu Leu Leu Ser Thr Gln
660 665 670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Phe Gly Ile Phe Arg Arg
675 680 685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
690 695 700

Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn
705 710 715 720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
649/735

755	760	765
Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu		
770	775	780
Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu		
785	790	795 800
Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp		
805	810	815
His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe		
820	825	830
Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln Arg Asp		
835	840	845
Lys Ile Tyr Val Phe		
850		

<210> 165

<211> 3138

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84).. (2648)

<400> 165

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gccactgccg ccctgccggg gcc atg ttc gct ctg ggc ttg ccc ttc ttg gtg 113

Met Phe Ala Leu Gly Leu Pro Phe Leu Val

1

5

10

ctc ttg gtg gcc tcg gtc gag agc cat ctg ggg gtt ctg ggg ccc aag 161

Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Val Leu Gly Pro Lys

15

20

25

aac gtc tcg cag aaa gac gcc gag ttt gag cgc acc tac gtg gac gag 209

Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu

30

35

40

gtc aac agc gag ctg gtc aac atc tac acc ttc aac cat act gtg acc 257

Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr

45

50

55

cgc aac agg aca gag ggc gtg cgt gtg tct gtg aac gtc ctg aac aag 305

Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys

60

65

70

cag aag ggg gcg ccg ttg ctg ttt gtg gtc cgc cag aag gag gct gtg 353

Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val

75

80

85

90

gtg tcc ttc cag gtg ccc cta atc ctg cga ggg atg ttt cag cgc aag 401
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg Lys

95 100 105

tac ctc tac caa aaa gtg gaa cga acc ctg tgt cag ccc ccc acc aag 449
 Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys

110 115 120

aat gag tcg gag att cag ttc ttc tac gtg gat gtg tcc acc ctg tca 497
 Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr Leu Ser

125 130 135

cca gtc aac acc aca tac cag ctc cgg gtc agc cgc atg gac gat ttt 545
 Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg Met Asp Asp Phe

140 145 150

gtg ctc agg act ggg gag cag ttc agc ttc aat acc aca gca gca cag 593
 Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln

155 160 165 170

ccc cag tac ttc aag tat gag ttc cct gaa ggc gtg gac tcg gta att 641
 Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu Gly Val Asp Ser Val Ile

175 180 185

gtc aag gtg acc tcc aac aag gcc ttc ccc tgc tca gtc atc tcc att 689
 Val Lys Val Thr Ser Asn Lys Ala Phe Pro Cys Ser Val Ile Ser Ile

190 195 200

cag gat gtg ctg tgt cct gtc tat gac ctg gac aac aac gta gcc ttc 737

Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe
205 210 215

atc ggc atg tac cag acg atg acc aag aag gcg gcc atc acc gta cag 785
Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln
220 225 230

cgc aaa gac ttc ccc agc aac agc ttt tat gtg gtg gtg gtg gtg aag 833
Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val Val Lys
235 240 245 250

acc gaa gac caa gcc tgc ggg ggc tcc ctg cct ttc tac ccc ttc gca 881
Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala
255 260 265

gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg 929
Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val
270 275 280

ctg gtg tct caa gca gtc acg tct gag gca tac gtc agt ggg atg ctc 977
Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu
285 290 295

ttt tgc ctg ggt ata ttt ctc tcc ttt tac ctg ctg acc gtc ctc ctg 1025
Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu
300 305 310

gcc tgc tgg gag aac tgg agg cag aag aag aag acc ctg ctg gtg gcc 1073
Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala
653/735

315	320	325	330	
att gac cga gcc tgc cca gaa agc ggt cac cct cga gtc ctg gct gat				1121
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala Asp				
	335	340	345	
tct ttt cct ggc agt tcc cct tat gag ggt tac aac tat ggc tcc ttt				1169
Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe				
	350	355	360	
gag aat gtt tct gga tct acc gat ggt ctg gtt gac agc gct ggc act				1217
Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr				
	365	370	375	
ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag cgg cgc				1265
Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg				
	380	385	390	
ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc				1313
Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser				
395	400	405	410	
ttt gaa cct gta ggt act cgg ccc cga gtg gac tcc atg agc tct gtg				1361
Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val				
	415	420	425	
gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat				1409
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn				
	430	435	440	
				654/735

gtc att cgc acc aag caa tac ctc tat gtg gct gac ctg gca cgg aag 1457

Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys

445

450

455

gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att 1505

Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile

460

465

470

gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc 1553

Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile

475

480

485

490

acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac 1601

Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr

495

500

505

tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac 1649

Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn

510

515

520

aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg 1697

Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu

525

530

535

ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc 1745

Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg

540

545

550

aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt 1793
 Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu
 555 560 565 570

ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct 1841
 Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala
 575 580 585

tgc tat cat gtg tgc ccc aac tat acc aat ttc cag ttt gac aca tcg 1889
 Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser
 590 595 600

ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag 1937
 Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys
 605 610 615

cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg 1985
 Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu
 620 625 630

gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg 2033
 Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly
 635 640 645 650

aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc 2081
 Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
 655 660 665

ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac 2129
 656/735

Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp

670

675

680

tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc 2177

Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile

685

690

695

cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc 2225

Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val

700

705

710

atg ggc aac gtc atc aac tgg tcg ctg gct gcc tat ggg ctt atc atg 2273

Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met

715

720

725

730

cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac 2321

Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn

735

740

745

ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg 2369

Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly

750

755

760

gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg 2417

Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val

765

770

775

gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg 2465

Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp

657/735

780

785

790

cag aaa acc cct gca gag tcg agg gag cac aac cgg gac tgc atc ctc 2513

Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu

795

800

805

810

ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc 2561

Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile

815

820

825

gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg 2609

Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly

830

835

840

tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg 2658

Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly

845

850

855

tccacacccc aggtgttgct gacactggat gacgacctgg atacttagaa aggggcttca 2718

ggaagggatg tgctgtttcc ctctacgtgc ccagtcctag cctcgctcta ggaccaggg 2778

ctggcttcta agtttccgtc cagtcttcag gcaagttctg tgtagtcat gcacacacat 2838

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658/735

tctgcttgaa gggctgggag atgaggtggg tctggatctt ttctcagagc gtctccatgc 3078

tatggttgca ttccgtttt ctatgaatga atttgcattc aataaacaac cagactcagt 3138

<210> 166

<211> 855

<212> PRT

<213> Homo sapiens

<400> 166

Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser Val

1 5 10 15

Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln Lys Asp

20 25 30

Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser Glu Leu Val

35 40 45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly

50 55 60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu

65 70 75 80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro

85 90 95

659/735

Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val

100

105

110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln

115

120

125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr

130

135

140

Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu

145

150

155

160

Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr

165

170

175

Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn

180

185

190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro

195

200

205

Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr

210

215

220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser

225

230

235

240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys

660/735

	245	250	255
Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp			
	260	265	270
Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val			
	275	280	285
Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe			
	290	295	300
Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp			
305	310	315	320
Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro			
	325	330	335
Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser			
	340	345	350
Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser			
	355	360	365
Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly			
	370	375	380
Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met			
385	390	395	400

Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr
405 410 415

Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
420 425 430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
435 440 445

Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
450 455 460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
465 470 475 480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
485 490 495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
500 505 510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
515 520 525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
530 535 540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu
545 550 555 560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr

565

570

575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro

580

585

590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala

595

600

605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn

610

615

620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe

625

630

635

640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile

645

650

655

Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln

660

665

670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg

675

680

685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro

690

695

700

Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn

663/735

705 710 715 720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
805 810 815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
820 825 830

Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser
835 840 845

Ser Cys Leu Leu Pro Cys Gly
850 855

<210> 167

<211> 2815

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56).. (571)

<400> 167

gcgaagcgcg cctgcgaccc ggcgtccggg cgcgctggag aggacgcgag gagcc atg 58

Met

1

agg cgc cag cct gcg aag gtg gcg gcg ctg ctg ctc ggg ctg ctc ttg 106

Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu

5

10

15

gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat 154

Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr

20

25

30

cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg 202

Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg

35

40

45

tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc 250

665/735

Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe
 50 55 60 65

ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc 298
 Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile
 70 75 80

cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat 346
 Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn
 85 90 95

gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag 394
 Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln
 100 105 110

ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct 442
 Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro
 115 120 125

gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc 490
 Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro
 130 135 140 145

cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct 538
 Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro
 150 155 160

ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca 591
 Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
 666/735

agaggagga caggagaggg cctttccctg gcctttctgt cttcgttgat gttcacttcc 651

aggaacggtc tcgtgggctg ctaagggcag ttctctgat atcctcacag caagcacage 711

tctctttcag gctttccatg gagtacaata tatgaactca cactttgtct cctctgttgc 771

ttctgtttct gacgcagtct gtgctctcac atggtagtgt ggtgacagtc cccgagggct 831

gacgtcctta cgggtggcgtg accagatcta cgggagagag actgagagga agaaggcagt 891

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agaagctggt ggagagacat tcaggagaga gcaagcccct tgtcatgttt ctgtctctgt 1131

tcatatccta aagatagact tctcctgcac cgccaggga gggtagcacg tgcagctctc 1191

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actaagcaaa tttatttaaa ttcattggaa atcacttctt gccccaaact gagacattgc 1311

atattgtgag ctcttggtct gatttggaga aaggactggt acccattttt ttggtgtggt 1371

tatggaagtg catgtagagc gtcctgccct ttgaaatcag actgggtgtg tgtcttcct 1431

ggacatcact gcctctccag ggcattctca ggcccggggg tctccttccc tcaggcagct 1491

ccagtgggtg gttctgaagg gtgctttcaa aacggggcac atctggctgg gaagtcacat 1551

ggactcttcc agggagagag accagctgag gcgtctctct ctgaggttgt gttgggtcta 1611

agcgggtgtg tgctgggctc caaggaggag gagcttgctg gggaaagaca ggagaagtac 1671

tgactcaact gcactgacca tgttgtcata attagaataa agaagaagtg gtcggaaatg 1731

cacattcctg gataggaatc acagctcacc ccaggatctc acaggtagtc tcctgagtag 1791

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ctgtatcacg gggaatgagg tgggggtgct tattttttaa tgaactaatc agagcctctt 1971

gagaaattgt tactcattga actggagcat caagacatct catggaagtg gatacggagt 2031

gatttggtgt ccatgctttt cactctgagg acatttaatc ggagaacctc ctggggaatt 2091

ttgtgggaga cacttgggaa caaaacagac accctgggaa tgcagttgca agcacagatg 2151

ctgccaccag tgtctctgac caccctggtg tgactgctga ctgccagcgt ggtacctccc 2211

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gacaactgcg tgggtccaaa cactcctctt cctccaggtc atttgttttg catttttaat 2331
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ataggcaccc aaaagtccgt gactaaattt cgtttgtctt tttgatagca aattatgtta 2451
agagacagtg atggctaggg ctcaacaatt ttgtattccc atgtttgtgt gagacagagt 2511
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cagagtaaac ttgaagcaga tctgtgcatg cttttcctct gcaacaattg gctcgtttct 2751
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gggc 2815

<210> 168

<211> 172

<212> PRT

<213> Homo sapiens

<400> 168

Met Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu

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15

Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu
20 25 30

Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser
35 40 45

Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp
50 55 60

Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe
65 70 75 80

Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
85 90 95

Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln
100 105 110

Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn
115 120 125

Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser
130 135 140

Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr
145 150 155 160

Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
670/735

<210> 169

<211> 3337

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136).. (1755)

<400> 169

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tacccgagtc tcgtttcctc tcagtccttc cacccttcat ggggccagag ccctctctcc 120

agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile

1

5

10

tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219

Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu

15

20

25

cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267

Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala

30

35

40

acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315

Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn

45

50

55

60

acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363

Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu

65

70

75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac 411

Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr

80

85

90

cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag 459

Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu

95

100

105

cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg 507

Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala

110

115

120

gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac 555

Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr

125

130

135

140

ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat 603

Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn

145

150

155

tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat	651
Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn	
160 165 170	
cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc	699
Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser	
175 180 185	
cct ctg acc tcc agc ggg cat cag gag cag gac aca gaa ctg ggc agt	747
Pro Leu Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser	
190 195 200	
acc cac aca gca ggt gcg acc tcc agc ctc aca cca tcc cgt ggg cct	795
Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro	
205 210 215 220	
gtg tct cca tct gtc tcc ttc cag ccc ctg gcc cgt tcc acc ccc agg	843
Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg	
225 230 235	
gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc	891
Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr	
240 245 250	
tcc ttc tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag	939
Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu	
255 260 265	
ggc aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc	987

Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser
270 275 280

agt ggg gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc 1035
Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr
285 290 295 300

acc ttg atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca 1083
Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro
305 310 315

gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc 1131
Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro
320 325 330

cct ggt gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa 1179
Pro Gly Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys
335 340 345

ttg ccc atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct 1227
Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro
350 355 360

act agc atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac 1275
Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp
365 370 375 380

ggg agc agc aga aat gag gag acc cca gca gct cca aca ccc gcc ggc 1323
Gly Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly
674/735

385

390

395

gcc act gga ggc agc tca gcc tgg cta gac agc agc tct gag aat agg 1371

Ala Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg

400

405

410

ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta 1419

Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val

415

420

425

gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc 1467

Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser

430

435

440

acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat 1515

Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr

445

450

455

460

aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc 1563

Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile

465

470

475

cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc 1611

Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly

480

485

490

ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc 1659

Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys

495

500

505

675/735

cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggg 1707
His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly

510

515

520

gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac 1755
Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His

525

530

535

540

tagtgaagcc ctgggctctt cccaccaccc atctgttccg ttcctgcagt atacctggcc 1815

cctctccgaa gcccctcttt ccctccctc tgggtctccat tctcttcagc tcctacatg 1875

ggctggggag gagacacctg gtgggcagag ctcaggcaga ggtttggatt tcagctccct 1935

cacttccggg gctgtgtggc ttiggcagat gtcagacttc tggctttgct tctccacgtg 1995

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ctggtagagc tgaggcatg agaggcagag tgcacagtgg tcaagggtgc agctctgcgg 2175

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tggcatttac caagggttgg atatatgtta ttatcactat taagtgttga ggtccaggc 2415

atgctgggca acagggaccc catctctaca aaaaagtta aaaaattagc caggcgtggt 2475

ggtgcacctg tcgtcttagc tacttgggag gctgaggtgg gaggatcgct tgagcccga 2535

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agaccctgtc tcaagaaaaa gaaaaatgca gagaaacagg agtcttggct actcctttag 2655

aggcagactc agaccctcct gcctcacagc tttatctttg tatttgcccc ttactttatc 2715

ttgtgccttg agaaattgct ggggagagag gtatgtccac tgggcagctg tacaggatgg 2775

aggatatagg gcgtttccac tcccagcagc caggttccct caccccaagc tcacccactg 2835

ttggggagat tatctacaat aacaccagaa acacattggg gtggattggg ggtatcctta 2895

tgggttcttt tcagggaacc attgctggac aaggcacagg agccacctcc atttctgagc 2955

tctgcaaggg acaagaacta gagccatcag gggctgggct cactgtggcc ccacccaag 3015

ccgtcagcct ccagggatct acaccctgcc ttggctgcta cagctttttc actccactgc 3075

cctaggggag ttcagcaacc taatgatctc tatctctgaa catctcttca tcccatgctc 3135

caagtccagc aacctgcacc ctggaaccag gagtggaccc taccggggt gtctgtatta 3195

atccccatcc cccaccacca atcttaaaaa gccctctgtc cccctaccct aaacccagt 3255

taggtaccca tgctgggcag gtcagttaac aatttatgca caggtagtag ttttatgtga 3315

ttaccgttcc agggtagctt tg 3337

<210> 170

<211> 540

<212> PRT

<213> Homo sapiens

<400> 170

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe

1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro

20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu

35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg

50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu

65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln

85 90 95

678/735

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
165 170 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
180 185 190

Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala
195 200 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
210 215 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
225 230 235 240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser
679/735

	245	250	255
Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly			
	260	265	270
Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu			
	275	280	285
Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro			
	290	295	300
Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser			
305	310	315	320
Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val			
	325	330	335
Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn			
	340	345	350
Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val			
	355	360	365
Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg			
	370	375	380
Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly			
385	390	395	400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser
405 410 415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
420 425 430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
435 440 445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
450 455 460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465 470 475 480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
485 490 495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
500 505 510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
515 520 525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
530 535 540

<210> 171

<211> 3579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (242)..(3094)

<400> 171

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gaggcccgag gcggaagtgg gacggccaag cagggaagcg agggctcggg atcgacggcc 120

gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccc 180

gggaaggagg cagggaagg ccgggcttgg gggcaggtgg tccgggcatc cagccttgaa 240

g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1

5

10

15

gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg 337

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

20

25

30

atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc 385

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35

40

45

ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc 433
 Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly

50

55

60

aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc 481
 Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys

65

70

75

80

atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac 529
 Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp

85

90

95

ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga 577
 Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly

100

105

110

gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag 625
 Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys

115

120

125

cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg 673
 Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu

130

135

140

gcg ctc tat cag aca gca att gaa agc gcc aga caa gct gga gac agc 721
 Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser

145

150

155

160

gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg 769
 Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
 165 170 175

ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg 817
 Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
 180 185 190

ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc 865
 Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
 195 200 205

cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc 913
 Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro
 210 215 220

agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca 961
 Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro
 225 230 235 240

ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct 1009
 Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro
 245 250 255

ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc 1057
 Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu
 260 265 270

cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc 1105
 684/735

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg

275

280

285

gtg gct aag agc ttt gat gct gtc ttg gag gcc ctg agc cgg ggt gag 1153

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu

290

295

300

ccc gtg gac ctc tcc tgc ctg ccc cct cca ccc gac cag ctg ccc cca 1201

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro

305

310

315

320

gac cca ccg tca cca ccg tcg cag cct ccg acc ccc gct acg gcg ccc 1249

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro

325

330

335

tcc aca aca gag gtg ccc cca ccc ccg agg acc ctg ctg gag gcg ctg 1297

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu

340

345

350

gag cag cgg atg gag cgg tac cag gtg gcc gca gcc cag gcc aag agc 1345

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser

355

360

365

aag ggg gac cag cgg aaa gct cga atg cac gag cgc atc gtc aag caa 1393

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln

370

375

380

tac caa gat gcc atc cga gcc cac aag gct ggc cga gcc gtg gat gtc 1441

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val

685/735

385	390	395	400	
gct gaa ttg ccc gtg ccc cca ggc ttc ccc cca atc cag ggc ctg gag				1489
Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu				
	405	410	415	
gcc acc aag ccc acc cag cag agt ctg gtg ggt gtc ctg gag act gcc				1537
Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala				
	420	425	430	
atg aag ctg gcc aac cag gat gaa ggc cca gag gat gaa gag gat gag				1585
Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu				
	435	440	445	
gtg cct aag aag cag aac agc cct gtg gcc ccc aca gcc cag ccc aaa				1633
Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys				
	450	455	460	
gcc cca ccc tca aga act ccc cag tcg gga tca gcc cca aca gcc aaa				1681
Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys				
465	470	475	480	
gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc				1729
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe				
	485	490	495	
cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag				1777
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys				
	500	505	510	

cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag	1825
Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys	
515 520 525	
gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac	1873
Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp	
530 535 540	
atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg	1921
Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu	
545 550 555 560	
gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat	1969
Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr	
565 570 575	
ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac	2017
Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn	
580 585 590	
cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag	2065
His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys	
595 600 605	
ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag	2113
Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys	
610 615 620	

caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa 2161
 Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
 625 630 635 640

agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac 2209
 Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
 645 650 655

atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga 2257
 Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
 660 665 670

ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat 2305
 Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
 675 680 685

ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac 2353
 Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
 690 695 700

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc 2401
 Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
 705 710 715 720

agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc 2449
 Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
 725 730 735

gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg 2497
 688/735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
740 745 750

aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg 2545
Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
755 760 765

gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg 2593
Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
770 775 780

gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag 2641
Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
785 790 795 800

acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg 2689
Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
805 810 815

ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc 2737
Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
820 825 830

cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc 2785
Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
835 840 845

agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc 2833
Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala
689/735

850	855	860	
ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac			2881
Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr			
865	870	875	880
cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag			2929
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln			
	885	890	895
ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag			2977
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln			
	900	905	910
ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc			3025
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser			
	915	920	925
agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt			3073
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser			
	930	935	940
gag ctg cag cgg ctc cgc agg tgaggagccc atggggcggg cagccccag			3124
Glu Leu Gln Arg Leu Arg Arg			
945	950		
aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca			3184
gacaatcagc ggacaatcgg ttctggactc acccctcattc cgggccccca gccccgccag			3244

agcctccgtg gctgcgggtg ttgggaacca tgcctgccag ccagtatgtg cccctcaccc 3304

aggcctggct gggccctgga gagtcctgtt tgcacagccc aggggtgtcc ggctcttggc 3364

ccgccccgga gcaggaggagg cggctggggc caagccccga gggcccctgc aagcacttta 3424

cttcctgttc ctccccagcc ttaaccccaa agccctcctg caccctaaag aagccactga 3484

ggctggccga gccacactgt ctccccaggg gcgtcgacct ggcccagctg ggtccccagg 3544

ccagcacatg gaataaaata gccaggcca cactc 3579

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<211> 951

<212> PRT

<213> Homo sapiens

<400> 172

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1

5

10

15

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

20

25

30

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35

40

45

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
50 55 60

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
65 70 75 80

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
85 90 95

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
100 105 110

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
115 120 125

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
130 135 140

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
145 150 155 160

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
165 170 175

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
180 185 190

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
195 200 205

Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro
210 215 220

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro
225 230 235 240

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro
245 250 255

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu
260 265 270

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg
275 280 285

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu
290 295 300

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro
305 310 315 320

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
325 330 335

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
340 345 350

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser
693/735

355	360	365
Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln		
370	375	380
Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val		
385	390	395 400
Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu		
405	410	415
Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala		
420	425	430
Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu		
435	440	445
Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys		
450	455	460
Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys		
465	470	475 480
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe		
485	490	495
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys		
500	505	510

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys
515 520 525

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp
530 535 540

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu
545 550 555 560

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
565 570 575

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
580 585 590

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys
595 600 605

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys
610 615 620

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
625 630 635 640

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
645 650 655

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
660 665 670
695/735

Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
675 680 685

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
690 695 700

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705 710 715 720

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
725 730 735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
740 745 750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
755 760 765

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
770 775 780

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
785 790 795 800

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
805 810 815

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
696/735

820	825	830
Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu		
835	840	845
Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala		
850	855	860
Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr		
865	870	875 880
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln		
885	890	895
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln		
900	905	910
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser		
915	920	925
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser		
930	935	940
Glu Leu Gln Arg Leu Arg Arg		
945	950	

<211> 2796

<212> DNA

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<221> CDS

<222> (574)..(1683)

<400> 173

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tagtccttaa caaagggaag gcgataaatg taaataagct cacattttca gaatgagcgg 180

tttgcagtaa ggagctgcgg cagcccagag tctgctcttt ttgggctggg ctaacctttc 240

cctgtttttt gttttttgtt ttgttttgtt ttgtttttt atggataaaa atatgcgctt 300

ccgaagtgcg agttgccagt ttacacgttt attagctaac tatctacagg catgagcaca 360

ttctctcatc tagcacactc tttcttgggc actcaattga ggaactctct gatcgtctgc 420

ctccagaaaa ttcatgatt atccaagtct cagataaatc tggtgccaga gtttggtttg 480

aactaactaa tgaagaaagc attctctact ggtcctcagt ctcaagagtg gtgaaccctt 540

gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594

Met Gly Asp Arg Arg Phe Ile

698/735

gac ttc caa ttc caa gat tta aat tca agt ctc aga ccc agg ttg gga 642

Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly

10

15

20

aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat 690

Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr

25

30

35

aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata 738

Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile

40

45

50

55

acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga 786

Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg

60

65

70

agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt 834

Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu

75

80

85

ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac 882

Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His

90

95

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tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc 930

Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu

105

110

115

acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat	978
Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp	
120 125 130 135	
cgt ttc cta gcc att gtc tat ccc ttc cga tcg cgt acc atc agg acc	1026
Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr	
140 145 150	
agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc	1074
Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu	
155 160 165	
agt ggt ggt att tca gct tct ttg ttc tcc acc act aat gtc aac aat	1122
Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn	
170 175 180	
gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca	1170
Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr	
185 190 195	
tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att	1218
Tyr Leu Ser Lys Ile Thr Ile Phe Ile Glu Val Val Gly Phe Ile Ile	
200 205 210 215	
cct ctg ata ttg aat gtt tct tgt tct tct gtg gtg ctt aga acc ctc	1266
Pro Leu Ile Leu Asn Val Ser Cys Ser Ser Val Val Leu Arg Thr Leu	
220 225 230	

cgc aag cct gca aca ttg tct cag att ggg acc aat aag aaa aaa gtg 1314

Arg Lys Pro Ala Thr Leu Ser Gln Ile Gly Thr Asn Lys Lys Lys Val

235

240

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ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta 1362

Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val

250

255

260

cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc 1410

Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala

265

270

275

att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att 1458

Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile

280

285

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295

acc ttg tgc ctt gca act ctg aat tgt tgc ttt gat cct ttt atc tat 1506

Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr

300

305

310

tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat 1554

Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His

315

320

325

ata agg atg gag tcg ctg ttt aag act gag aca cct ctg acc ccc aaa 1602

Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys

330

335

340

cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat 1650

701/735

Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn

345

350

355

aat ggt ggt gaa tta atg ctg gaa tcc acc ttc taggtaccag aattgtcttt 1703

Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe

360

365

370

caggttcagc tacagtgtct cttatgattt ttttcctatg ctataaatag gagaaacaaa 1763

ttgaagctaa tgatactgag aatagagtaa tgtaccaaatt gcagtcagat acatttgttt 1823

gaacactatt gtacatatc tgttttgttc agtaattata ggtcaagtct aattacaaca 1883

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cttgactttt agtgaatgga ggggttattt taaacttaaa aaaaaaggca ttccagtaat 2003

tttggttaatt gggttgggcc tataaatata gaacaaattc agggattatt taaaaacatc 2063

tgtgttacta ctgatatatg ctagtatttt tttccttttt tgaattaata ttgaatttat 2123

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ttgaatttta aaatattggc aaattttacc tagattttta aaacctaat gaagtgttg 2243

aatgaatatg ggtgggaaat ttggaattta gacaacattt acgcatttat aataaccaca 2303

attagtgtca gcttttaaaa ctttcttttt aaaataattc tagaattttc atatgaaatt 2363

gttaatcctg aaagtgcta cttatgtgcc tggcaggtat aaaatggaaa actcataaaa 2423

ttaacagtgt caatttaaaa aaaaaaaaaac ttttaagcaac actatattat ttcttaagat 2483

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aagatgtgta cat 2796

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<211> 370

<212> PRT

<213> Mus musculus

<400> 174

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20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe
50 55 60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn
65 70 75 80

Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
85 90 95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
100 105 110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
115 120 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
130 135 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
145 150 155 160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
165 170 175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
180 185 190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
195 200 205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
210 215 220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225 230 235 240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
245 250 255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
260 265 270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe
275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305 310 315 320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr
325 330 335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
705/735

340

345

350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser

355

360

365

Thr Phe

370

<210> 175

<211> 2299

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (67)..(1176)

<400> 175

cctaccggtc catagtgtca gagtgggtgaa cccctgcagc cagcaggcct cctgaaaaaa 60

aagtcc atg ggt gac aga aga ttc att gac ttc caa ttc caa gat tca 108

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser

1

5

10

aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act 156

Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr

15

20

25

30

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tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac 204
 Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr

35 40 45

agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt 252
 Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe

50 55 60

gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc 300
 Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile

65 70 75

acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt 348
 Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe

80 85 90

aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc 396
 Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu

95 100 105 110

tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg 444
 Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met

115 120 125

ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat 492
 Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr

130 135 140

cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg	540
Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val	
145 150 155	
tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct	588
Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser	
160 165 170	
ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa	636
Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu	
175 180 185 190	
ggc ttc tcc aaa cgt gtc tgg aag act tat tta tcc aag atc aca ata	684
Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile	
195 200 205	
ttt att gaa gtt gtt ggg ttt atc att cct cta ata ttg aat gtc tct	732
Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser	
210 215 220	
tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct	780
Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser	
225 230 235	
caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat	828
Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His	
240 245 250	
atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc	876

Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe
 255 260 265 270

ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa 924
 Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu
 275 280 285

aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg 972
 Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu
 290 295 300

aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt 1020
 Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe
 305 310 315

cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt 1068
 Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe
 320 325 330

aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa 1116
 Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln
 335 340 345 350

gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta 1164
 Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu
 355 360 365

gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc 1216
 Glu Ser Thr Phe

ctataatfff tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc 1276

accaaatacca gtcagatata ttgttttgaa ggtatactgt agagttttta ttgctgtttt 1336

gttcagtaat tataggtcaa atctaattac aacaaccaag atggattgcc aaactcttct 1396

gcttggttgg aatttcattg tatcgatta tccaggtggc tagtggcatt tgataatata 1456

gagatgactt tgaaactttc aaaaaggtat ttctattcca atgatatttg gtaattaggt 1516

tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgtta ctactgatat 1576

atgctagttt tattttattt ttttggactg tcattgagtt tatttttagca caagaatatt 1636

tttagcctaa cattattaat aagaaatgtg tcaaattttt aacattggta aaatatgtta 1696

tgtgcatfff gaaaacagaa aacaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756

aaaattaaca ggatttacac aattataatc accagcagtg tgagttttaa aaacttcgtt 1816

gtttttacac caaattaaaa ttttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876

gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936

tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056

ctgcatttgt gccaggtca ggagcaaatt gaaaaaaaaa ataaagtaat actaaaaaat 2116

caaactataa acccaaaaca ttattataaa cctgaattaa tccttttttg aggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttgagc ctaatatagc 2236

caggagctgc tgaatttgtg cccctggatt ggaaccaaatt aaaaaaaaaa aaaaaaaatt 2296

cct 2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser

1 5 10 15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val

35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe

50 55 60

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Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn
65 70 75 80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
85 90 95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
100 105 110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
115 120 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
130 135 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
145 150 155 160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
165 170 175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
180 185 190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
195 200 205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
712/735

210	215	220	
Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile			
225	230	235	240
Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala			
	245	250	255
Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr			
	260	265	270
Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe			
	275	280	285
Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys			
	290	295	300
Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys			
305	310	315	320
Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr			
	325	330	335
Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu			
	340	345	350
Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser			
	355	360	365

Thr Phe

370

<210> 177

<211> 973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (30)..(416)

<400> 177

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Met Ala Arg Gly Ser Leu Arg Arg

1

5

ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc 101

Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser

10

15

20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc 149

Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser

25

30

35

40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg 197

Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg

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45

50

55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct 245

Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro

60

65

70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg 293

Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu

75

80

85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc 341

Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys

90

95

100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag 389

Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu

105

110

115

120

ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccctgcc 436

Gly Cys Pro Ala Val Ala Leu Ile Gln

125

gccggggctc gcccaactcat cattcattca tccattctag agccagtctc tgcctcccag 496

acgcggcggg agccaagctc ctccaaccac aaggggggtg gggggcggtg aatcacctcc 556

gaggcctggg tccagggttc aggggaacct tccaagggtg ctggttgccc tgcctctggc 616

tccagaacag aaaggagcc tcacgtggc tcacacaaaa cagctgacac tgactaagga 676

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actgcagcat ttgcacaggg gaggggggtg ccctccttcc tagaggccct gggggccagg 736

ctgacttggg gggcagactt gacactaggg ccactcact cagatgtcct gaaattccac 796

cacgggggtc accctggggg gttagggacc tatttttaac actagggggc tggcccacta 856

ggagggctgg ccctaagata cagaccccc ccaactccca aagcggggag gagatattta 916

ttttggggag agtttggagg ggaggagaa tttattaata aaagaatctt taacttt 973

<210> 178

<211> 129

<212> PRT

<213> Homo sapiens

<400> 178

Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly

1 5 10 15

Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly

20 25 30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys

35 40 45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys

50 55 60

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Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
65 70 75 80

Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
85 90 95

Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
100 105 110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
115 120 125

Gln

<210> 179

<211> 3631

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (191).. (3244)

<400> 179

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ggcgctggcg caagatgatg ttgtccata ttttaaaacg gagccaggcc taccacagat 120

ccacctggaa gggaaccgcc ttgttctcac ctgccttgcc gaaggagct ggcctttgga 180

gttcaagtgg atg cgc gat gac agt gag ctc acc acc tac agc agc gaa 229

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu

1

5

10

tat aag tac att att cca tct ttg cag aag ctc gat gct ggg ttt tac 277

Tyr Lys Tyr Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr

15

20

25

cgc tgc gtg gtg cga aac aga atg gga gca ctc ctg caa aga aaa tca 325

Arg Cys Val Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser

30

35

40

45

gaa gtt caa gtc gca tat atg gga agt ttc atg gat acg gac cag agg 373

Glu Val Gln Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg

50

55

60

aaa aca gtt tct caa gga cgt gca gcg att cta aac ctg ctg ccc atc 421

Lys Thr Val Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile

65

70

75

acc agc tac ccc aga cct caa gtg act tgg ttt aga gaa ggg cac aag 469

Thr Ser Tyr Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys

80

85

90

att att cca agc aac aga ata gcc atc aca ttg gag aat cag ctg gtg 517

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Ile Ile Pro Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val

95

100

105

atc ctc gcc acc aca acc agt gat gcc ggg gca tac tac gtg cag gcc 565

Ile Leu Ala Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala

110

115

120

125

gtg aat gag aaa aat gga gaa aac aag aca agc cca ttc att cat ttg 613

Val Asn Glu Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu

130

135

140

agc ata gca aga gat gtt ggc aca cct gaa acc atg gcc cca acc att 661

Ser Ile Ala Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile

145

150

155

gtg gtt ccc ccg ggc aac aga agt gtg gtg gct gga tcc agt gag acc 709

Val Val Pro Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr

160

165

170

acc ttg gaa tgt ata gcc agt gcc agg cct gtg gag gac ctg agt gtg 757

Thr Leu Glu Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val

175

180

185

acc tgg aag agg aat gga gtg aga atc acc agt ggc ctc cac agc ttt 805

Thr Trp Lys Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe

190

195

200

205

gga aga cgc ctc acc atc agc aac ccg acg tcc gcg gac acc ggg cca 853

Gly Arg Arg Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro

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210	215	220	
tac gtc tgc gag gcg gcg ctg ccg ggg agc gct ttt gaa ccg gcc agg			901
Tyr Val Cys Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg			
225	230	235	
gcg acg gcc ttt ctt ttc atc ata gag cca cca tat ttt act gct gag			949
Ala Thr Ala Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu			
240	245	250	
ccc gag agt cgg att tca gct gaa gta gaa gaa act gtg gac atc gga			997
Pro Glu Ser Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly			
255	260	265	
tgt caa gcc atg ggg gtc ccc ctt ccc acc ctc cag tgg tac aag gat			1045
Cys Gln Ala Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp			
270	275	280	285
gcc atc tcc atc agc agg ctc cag aat cct cga tac aaa gtg ctc gcc			1093
Ala Ile Ser Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala			
290	295	300	
agc gga ggc ctg cgc atc cag aag ctg cgt cca gag gac tcc gga atc			1141
Ser Gly Gly Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile			
305	310	315	
ttc cag tgc ttc gcc agc aat gaa gga ggg gag atc cag acc cac acc			1189
Phe Gln Cys Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr			
320	325	330	

tac ctg gat gta acc aat atc gct cca gtg ttc acc cag cgg cca gtg 1237

Tyr Leu Asp Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val

335

340

345

gac acc aca gtt act gac ggg atg aca gcc att cta agg tgt gag gtg 1285

Asp Thr Thr Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val

350

355

360

365

tcc ggg gct ccc aaa ccc gcc atc acc tgg aaa aga gaa aac cac att 1333

Ser Gly Ala Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile

370

375

380

ctg gcc agt ggc tct gtc cgg att cct agg ttc atg ctt ctt gaa tcg 1381

Leu Ala Ser Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser

385

390

395

ggg ggt cta cag atc gcg ccc gtc ttc atc cag gat gcc ggc aac tac 1429

Gly Gly Leu Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr

400

405

410

acc tgc tat gcg gcc aac aca gag ggc tcc ctg aat gca tcg gcc acg 1477

Thr Cys Tyr Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr

415

420

425

ctc act gtg tgg aat cgg acg tcc atc gtc cac cct cct gag gac cac 1525

Leu Thr Val Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His

430

435

440

445

gtg gtg att aag ggg acc acg gcc acg ctg cac tgt ggt gcc aca cat 1573
 Val Val Ile Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His

450

455

460

gac ccc cgg gtt tca ctc cgc tac gtt tgg aag aag gac aac gtg gcc 1621
 Asp Pro Arg Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala

465

470

475

ctg act cca tcg agc acg tct agg atc gtg gtg gag aag gac ggg tcc 1669
 Leu Thr Pro Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser

480

485

490

ctt ctc atc agc cag acg tgg tca ggc gac atc ggt gac tac agc tgc 1717
 Leu Leu Ile Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys

495

500

505

gag att gtt tct gaa gga ggg aat gac tcc agg atg gcc cgg ctg gaa 1765
 Glu Ile Val Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu

510

515

520

525

gtg att gaa ctg cct cat tca cct cag aac ctc ctg gtc agc cct aat 1813
 Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn

530

535

540

tct tcc cac agc cac gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat 1861
 Ser Ser His Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp

545

550

555

gga aac agt cct att ctt tat tac atc gtg gag ctg tct gaa aac aac 1909

Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn

560

565

570

tct cca tgg aag gtg cat ctg tca aac gtt ggc cct gag atg aca ggc 1957

Ser Pro Trp Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly

575

580

585

gtc acc gtg agt ggc ctg act ccg gct cgt acc tat caa ttc cgg gtg 2005

Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val

590

595

600

605

tgc gcg gtg aat gaa gtg ggc agg ggc cag tac agt gcc gag aca agc 2053

Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser

610

615

620

agg ttg atg cta cct gaa gaa cca ccc agt gct ccc ccg aaa aat ata 2101

Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile

625

630

635

gtg gcc agt ggg cgg act aat cag tcc att atg gtc cag tgg cag cca 2149

Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro

640

645

650

ccc cca gaa aca gag cac aac ggg gtg ttg cgt gga tac atc ctc agg 2197

Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg

655

660

665

tac cgc ctg gct ggc ctt ccc gga gag tac cag cag cgg aac atc acc 2245

Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr

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670

675

680

685

agc ccg gag gtg aac tac tgc ctg gtg aca gac ctg atc atc tgg aca 2293

Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr

690

695

700

cag tat gag ata cag gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc 2341

Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val

705

710

715

ttc agc agg gca gtg acc gag tac acc ttg cag gga gtg ccc acc gcg 2389

Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala

720

725

730

ccc ccg cag aac gtg cag acg gaa gcc gtg aac tcc acc acc att cag 2437

Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln

735

740

745

ttc ctg tgg aac cct ccg cct cag cag ttt atc aat ggc atc aac cag 2485

Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln

750

755

760

765

gga tac aag ctt ctg gca tgg ccg gca gat gcc ccc gag gct gtc act 2533

Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr

770

775

780

gtg gtc act att gcc cca gat ttc cac gga gtc cac cat gga cac ata 2581

Val Val Thr Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile

785

790

795

724/735

acg aac ctg aag aag ttt acc gcc tac ttc act tcc gtt ctg tgc ttc 2629

Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe

800

805

810

acc acc cct ggg gac ggg cct ccc agc aca cct cag ctg gtc tgg act 2677

Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr

815

820

825

cag gaa gac aaa cca gga gct gtg gga cat ctg agt ttc aca gag atc 2725

Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile

830

835

840

845

ttg gac aca tct ctc aag gtc agc tgg cag gag ccc ctg gag aaa aat 2773

Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn

850

855

860

ggc atc att act ggc tat cag atc tct tgg gaa gtg tac ggc agg aac 2821

Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn

865

870

875

gac tct cgt ctc acg cac acc ctg aac agc acg acg cac gag tac aag 2869

Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys

880

885

890

atc caa ggc ctc tca tct ctc acc acc tac acc atc gac gtg gcc gct 2917

Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala

895

900

905

gtg act gcc gtg ggc act ggc ctg gtg act tca tcc acc att tct tct 2965
Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser
910 915 920 925

gga gtg ccc cca gac ctt cct ggt gcc cca tcc aac ctg gtc att tcc 3013
Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser
930 935 940

aac atc agc cct cgc tcc gcc acc ctt cag ttc cgg cca ggc tat gac 3061
Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp
945 950 955

ggg aaa acg tcc atc tcc agg tgg att gtt gag ggg cag atg aga cat 3109
Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His
960 965 970

caa ggt gtt gga tta cct gcc gag gtc aca cag cca agc cat gaa gcc 3157
Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala
975 980 985

gga ttg gag cct gca aac ctc gga agt ctg tgg ctg ctc agc ctg gtg 3205
Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val
990 995 1000 1005

tat tgg tgt tac agc cag aaa ctt tgg gaa ttc tct tgt tagttgggta 3254
Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys
1010 1015

gttttactgt aattttctat aaagaattca tatcatctgt taatggcgac agtttttggtt 3314
726/735

tcttccttg aatttttat attcttctt tctcttttt gtttcttctt ctttgagtat 3374

tttgtaatct tactgggagg gctaaagcgt cttctatcat atcgaattgg gacaatgata 3434

gaagacaatc ttigtittgt cactctaaag aaattattgt aagattttat catcaggtat 3494

gacatttaca ccattgatgt aggcctttta aaaaatatat ccagcctgta ttgggttaag 3554

atgattcttt tctgatcctg atttcctagg agttgggttt tttttttta aagcataaat 3614

aaatttaatt gcatcag 3631

<210> 180

<211> 1018

<212> PRT

<213> Homo sapiens

<400> 180

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu Tyr Lys Tyr

1 5 10 15

Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr Arg Cys Val

20 25 30

Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser Glu Val Gln

35 40 45

Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg Lys Thr Val
50 55 60

Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile Thr Ser Tyr
65 70 75 80

Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys Ile Ile Pro
85 90 95

Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val Ile Leu Ala
100 105 110

Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala Val Asn Glu
115 120 125

Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu Ser Ile Ala
130 135 140

Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile Val Val Pro
145 150 155 160

Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr Thr Leu Glu
165 170 175

Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val Thr Trp Lys
180 185 190

Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe Gly Arg Arg
195 200 205

Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro Tyr Val Cys
210 215 220

Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg Ala Thr Ala
225 230 235 240

Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu Pro Glu Ser
245 250 255

Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly Cys Gln Ala
260 265 270

Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp Ala Ile Ser
275 280 285

Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala Ser Gly Gly
290 295 300

Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile Phe Gln Cys
305 310 315 320

Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr Tyr Leu Asp
325 330 335

Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val Asp Thr Thr
340 345 350

Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val Ser Gly Ala
729/735

355

360

365

Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile Leu Ala Ser

370

375

380

Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser Gly Gly Leu

385

390

395

400

Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr Thr Cys Tyr

405

410

415

Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr Leu Thr Val

420

425

430

Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His Val Val Ile

435

440

445

Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His Asp Pro Arg

450

455

460

Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala Leu Thr Pro

465

470

475

480

Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser Leu Leu Ile

485

490

495

Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys Glu Ile Val

500

505

510

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Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu Val Ile Glu
515 520 525

Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His
530 535 540

Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser
545 550 555 560

Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp
565 570 575

Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val
580 585 590

Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val
595 600 605

Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met
610 615 620

Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser
625 630 635 640

Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu
645 650 655

Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu
660 665 670

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Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu
675 680 685

Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu
690 695 700

Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg
705 710 715 720

Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln
725 730 735

Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp
740 745 750

Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys
755 760 765

Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr
770 775 780

Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu
785 790 795 800

Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro
805 810 815

Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp
732/735

820

825

830

Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr

835

840

845

Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile

850

855

860

Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg

865

870

875

880

Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly

885

890

895

Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala

900

905

910

Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro

915

920

925

Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser

930

935

940

Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr

945

950

955

960

Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val

965

970

975

Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu
980 985 990

Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys
995 1000 1005

Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys
1010 1015

<210> 181

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 181

cttctgctct aaaagctgcg

20

<210> 182

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 182

cgacctgcag ctcgagcaca

20

735/735